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 NEWS 3  APR 02  PATDPAFULL: Application and priority number formats enhanced
 NEWS 4  APR 02  DWPI: New display format ALLSTR available
 NEWS 5  APR 02  New Thesaurus Added to Derwent Databases for Smooth Sailing through U.S. Patent Codes
 NEWS 6  APR 02  EMBASE Adds Unique Records from MEDLINE, Expanding Coverage back to 1948
 NEWS 7  APR 07  CA/CAplus CLASS Display Streamlined with Removal of Pre-IPC 8 Data Fields
 NEWS 8  APR 07  50,000 World Traditional Medicine (WTM) Patents Now Available in CAplus
 NEWS 9  APR 07  MEDLINE Coverage Is Extended Back to 1947
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 NEWS 20 SEP 09  New basic patent number increases precision in retrieving records from USGENE

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REVISED CLASS FIELDS (/NCL) LAST RELOADED:  Jun 2010
USPTO MANUAL OF CLASSIFICATIONS THESAURUS ISSUE DATE:  Jun 2010

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substance identification.

=> s auxotroph?/bi,ab      7899 AUXOTROPH?/BI
7284 AUXOTROPH?/AB
L1        7899 AUXOTROPH?/BI,AB

=> s (presen? or absen? or test?)/bi,ab   5450589 PRESEN?/BI
5188538 PRESEN?/AB                 602214 ABSEN?/BI
578446 ABSEN?/AB                  2439483 TEST?/BI
2272033 TEST?/AB
L2     7638966 (PRESEN? OR ABSEN? OR TEST?)/BI,AB
 95% OF LIMIT FOR TOTAL ANSWERS REACHED

=> s l1 and l2
L3        2881 L1 AND L2
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=> s l3 and (yeast? or saccharomyces or cerevisiae)/bi,ab
256043 YEAST?/BI 215568 YEAST?/AB
107676 SACCHAROMYCES/BI 62234
SACCHAROMYCES/AB 100200 CEREVISIAE/BI
67335 CEREVISIAE/AB
L4 632 L3 AND (YEAST? OR SACCHAROMYCES OR
CEREVISIAE)/BI,AB

=> s l4 not 2010/py 1273554 2010/PY
L5 614 L4 NOT 2010/PY

=> l5 not 2009/py
L5 IS NOT A RECOGNIZED COMMAND
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=> s l5 not 2009/py 1886072 2009/PY
L6 591 L5 NOT 2009/PY

=> s l6 not 2008/py 1804885 2008/PY
L7 569 L6 NOT 2008/PY

=> s l7 not 2007/py 1726215 2007/PY
L8 547 L7 NOT 2007/PY

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(FILE 'HOME' ENTERED AT 12:04:56 ON 17 SEP 2010)
FILE 'CAPLUS' ENTERED AT 12:05:31 ON 17 SEP 2010
L1 7899 S AUXOTROPH?/BI,AB
L2 7638966 S (PRESEN? OR ABSEN? OR TEST?)/BI,AB
L3 2881 S L1 AND L2
L4 632 S L3 AND (YEAST? OR SACCHAROMYCES OR
CEREVISIAE)/BI,AB
L5 614 S L4 NOT 2010/PY
L6 591 S L5 NOT 2009/PY
L7 569 S L6 NOT 2008/PY
L8 547 S L7 NOT 2007/PY

=> s (auxotroph? (10a) (yeast? or saccharomyces or
cerevisiae))/bi,ab 7899 AUXOTROPH?/BI 7284
AUXOTROPH?/AB 256043 YEAST?/BI
215568 YEAST?/AB 107676 SACCHAROMYCES/BI
62234 SACCHAROMYCES/AB 100200 CEREVISIAE/BI
67335 CEREVISIAE/AB
L9 840 (AUXOTROPH? (10A) (YEAST? OR
SACCHAROMYCES OR CEREVISIAE))/BI,AB

=> s l2 and l9
L10 271 L2 AND L9

=> s l10 not 2010/py 1273554 2010/PY
L11 261 L10 NOT 2010/PY

=> s l11 not 2009/py 1886072 2009/PY
L12 252 L11 NOT 2009/PY

=> s l12 2008/py
MISSING OPERATOR L12 2008/PY
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=> s l12 not 2008/py 1804885 2008/PY
L13 242 L12 NOT 2008/PY

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L15 222 L14 NOT 2006/PY

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=> s l16 not 2004/py 1353918 2004/PY
L17 196 L16 NOT 2004/PY

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L1 7899 S AUXOTROPH?/BI,AB
L2 7638966 S (PRESEN? OR ABSEN? OR TEST?)/BI,AB
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CEREVISIAE)/BI,AB
L5 614 S L4 NOT 2010/PY
L6 591 S L5 NOT 2009/PY
L7 569 S L6 NOT 2008/PY
L8 547 S L7 NOT 2007/PY
L9 840 S (AUXOTROPH? (10A) (YEAST? OR
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L11 261 S L10 NOT 2010/PY
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L14 234 S L13 NOT 2007/PY
L15 222 S L14 NOT 2006/PY
L16 208 S L15 NOT 2005/PY
L17 196 S L16 NOT 2004/PY

=> d l17 1-196 bib ab

L17 ANSWER 1 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2004:10572 CAPLUS <<LOGINID::20100917>>
DN 140:194224
TI Cloning and sequence analysis of the TRP1 gene encoding the phosphoribosyl anthranilate isomerase from Pichia anomala (strain K)
AU Friel, Damien; Vandenbol, Micheline; Jijakli, M. Haissam
CS Plant Pathology Unit, University of Agricultural Sciences, Gembloux, 5030, Belg.
SO Yeast (2003), 20(16), 1331-1337 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB Pichia anomala (strain K) is an efficient biocontrol agent against post-harvest diseases affecting apples. To study the role of strain K genes in biocontrol activity, it is useful to identify selectable markers on which to base a gene disruption strategy. The Pichia anomala TRP1 gene (PaTRP1) was isolated by complementation of the multi- ***auxotrophic*** S. ***cerevisiae*** strain FY-1679-18b. DNA sequence anal. revealed the ***presence*** of a 699 bp ORF encoding a 233 amino acid protein showing the typical conserved structure of proteins of the phosphoribosyl anthranilate isomerase (PRAI) family. Codon anal. revealed a high no. of unused codons. Downstream from PaTRP1 was found the 3' extremity of a gene highly similar to the IPP1 gene (coding for the inorg. pyrophosphatase). In addn., a sequence of the 5' extremity of

the insert is highly similar to a fragment of the S. cerevisiae PRP9 gene, coding for a spliceosome-assocd. protein. The nucleotide sequence has been deposited in the Genbank database under Accession No. AY198188.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)
RE.CNT 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 2 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:995036 CAPLUS <<LOGINID::20100917>>
DN 140:141561
TI The human phosphatidylinositol phosphatase SAC1 interacts with the coatomer I complex
AU Rohde, Holger M.; Cheong, Fei Ying; Konrad, Gerlinde; Paiha, Karin; Mayinger, Peter; Boehmelt, Guido
CS Boehringer Ingelheim Austria GmbH, Vienna, 1121, Austria
SO Journal of Biological Chemistry (2003), 278(52), 52689-52699 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB The Saccharomyces cerevisiae SAC1 gene encodes an integral membrane protein of the endoplasmic reticulum (ER) and the Golgi app. ***Yeast*** SAC1 mutants display a wide array of phenotypes including inositol ***auxotrophy*** , cold sensitivity, secretory defects, disturbed ATP transport into the ER, or suppression of actin gene mutations. At ***present*** , it is not clear how these phenotypes relate to the finding that SAC1 displays polyphosphoinositide phosphatase activity. Moreover, it is still an open question whether SAC1 functions similarly in mammalian cells, since some phenotypes are yeast-specific. Potential protein interaction partners and, connected to that, possible regulatory circuits have not been described. Therefore, we have cloned human SAC1 (hSAC1), show that it behaves similar to ySac1p in terms of substrate specificity, demonstrate that the endogenous protein localizes to the ER and Golgi, and identify for the first time members of the coatomer I (COPI) complex as interaction partners of hSAC1. Mutation of a putative COPI interaction motif (KXKXX) at its C terminus abolishes interaction with COPI and causes accumulation of hSAC1 in the Golgi. In addn., we generated a catalytically inactive mutant, demonstrate that its lipid binding capacity is unaltered, and show that it accumulates in the Golgi, incapable of interacting with the COPI complex despite the ***presence*** of the KXKXX motif. These results open the possibility that the enzymic function of hSAC1 provides a switch for accessibility of the COPI interaction motif.
OSC.G 19 THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 3 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2003:620748 CAPLUS <<LOGINID::20100917>>
DN 139:258045
TI Weak organic acid stress inhibits aromatic amino acid uptake by ***yeast*** , causing a strong influence of amino acid ***auxotrophies*** on the phenotypes of membrane transporter mutants
AU Bauer, Bettina E.; Rossington, Danielle; Mollapour, Mehdi; Mamnun, Yasmine; Kuchler, Karl; Piper, Peter W.
CS Department of Molecular Genetics, University and BioCenter of Vienna, Austria
SO European Journal of Biochemistry (2003), 270(15), 3189-3195 CODEN: EJBCAI; ISSN: 0014-2956
PB Blackwell Publishing Ltd.
DT Journal
LA English
AB The ability of yeasts to grow in the ***presence*** of weak org. acid preservatives is an important cause of food spoilage. Many of the determinants of acetate resistance in Saccharomyces cerevisiae differ from the determinants of resistance to the more lipophilic sorbate and benzoate. Interestingly, we show in this study that hypersensitivity to both acetate and sorbate results when the cells have auxotrophic requirements for arom. amino acids. In tryptophan biosynthetic pathway mutants, this weak acid hypersensitivity is suppressed by supplementing the medium with high levels of tryptophan or, in the case of sorbate sensitivity, by overexpressing the Tat2p high affinity tryptophan permease. Weak acid stress therefore inhibits uptake of arom. amino acids from the medium. This allows auxotrophic requirements for these amino acids to strongly influence the resistance phenotypes of mutant strains. This property must be taken into consideration when using these phenotypes to attribute functional assignments to genes. We show that the acetate sensitivity phenotype previously ascribed to yeast mutants lacking the Pdr12p and Azr1p plasma membrane transporters is an artifact arising from the use of trp1 mutant strains. These transporters do not confer resistance to high acetate levels and, in prototrophs, their ***presence*** is actually detrimental for this resistance.
OSC.G 29 THERE ARE 29 CAPLUS RECORDS THAT CITE THIS RECORD (29 CITINGS)
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 4 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:671095 CAPLUS <<LOGINID::20100917>>
DN 137:334781
TI High-throughput global peptide proteomic analysis by combining stable isotope amino acid labeling and data-dependent multiplexed-MS/MS
AU Berger, Scott J.; Lee, Sang-Won; Anderson, Gordon A.; Pasa-Tolic, Liljana; Tolic, Nikola; Shen, Yufeng; Zhao, Rui; Smith, Richard D.
CS Environmental Molecular Sciences Laboratory, Pacific Northwest National Laboratory, Richland, WA, 99352, USA
SO Analytical Chemistry (2002), 74(19), 4994-5000 CODEN: ANCHAM; ISSN: 0003-2700
PB American Chemical Society
DT Journal
LA English
AB In this work, we describe the application of a stable isotope amino acid (lysine) labeling in conjunction with data-dependent multiplexed tandem mass spectrometry (MS/MS) to facilitate the characterization and identification of peptides from proteomic (global protein) digests. Lysine ***auxotrophic*** ***yeast*** was grown in the ***presence*** of 13C-labeled or unlabeled lysine and combined after harvesting in equal proportions. Endoproteinase LysC digestion of the cytosolic fraction produced a global proteomic sample, consisting of heavy/light labeled peptide pairs. Then data-dependent multiplexed-MS/MS was applied to simultaneously select and dissoc. only labeled peptide ion pairs. The approach allows differentiation between N-terminal (e.g., b-type ions) and C-terminal fragment ions (e.g., y-type ions) in resulting tandem mass spectra, as well as the capability of differentiation between near-isobaric glutamine and lysine residues. We also describe

the utility of peptide compn. and fragment information to support peptide identifications and examine the potential application of lysine labeling for differential quant. protein anal.
OSC.G 50 THERE ARE 50 CAPLUS RECORDS THAT CITE THIS RECORD (50 CITINGS)
RE.CNT 26 THERE ARE 26 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 5 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:389565 CAPLUS <<LOGINID::20100917>>
DN 137:108385
TI Stability studies of recombinant Saccharomyces cerevisiae in the ***presence*** of varying selection pressure
AU Gupta, Jagdish C.; Mukherjee, K. J.
CS Centre for Biotechnology, Jawaharlal Nehru University, New Delhi, 110 067, India
SO Biotechnology and Bioengineering (2002), 78(5), 475-488 CODEN: BIBIAU; ISSN: 0006-3592
PB John Wiley & Sons, Inc.
DT Journal
LA English
AB A recombinant ***yeast*** plasmid carrying the leu2 gene for ***auxotrophic*** complementation and a reporter gene for .beta.-galactosidase under the control of Gal10 promoter was studied in Saccharomyces cerevisiae. Growth, product formation, and plasmid stability were studied in defined, semi-defined, and complex media. The biomass concn. and specific activity were higher in complex medium than in defined medium, which was selective for the growth of plasmid-contg. cells, leading to a 10-fold increase in volumetric activity. However, plasmid instability was very high in complex media with 50% plasmid-free cells emerging in the culture within 75 h of cultivation. In order to control instability, the growth rates of the plasmid-contg. and plasmid-free cells were detd. in semi-defined media, which consisted of defined medium supplemented with different concns. of yeast ext. Below a crit. concn. of yeast ext. (0.05 g/L), the plasmid-contg. cells had a growth rate advantage over the plasmid-free cells. This was possibly because, at this concn. of yeast ext., the availability of leucine became the rate-detg. factor in the specific growth rate of plasmid-free cells. A feeding strategy was designed which maintained a low concn. of the residual yeast ext. in the medium and thus continuously provided the plasmid-contg. cells with a competitive advantage over the plasmid-free cells. This resulted in high stability as well as high cell d. under non-selective conditions, which led to a 10-fold increase in the volumetric activity compared to that achieved in defined selective media. A simple math. model was formulated to verify the exptl. data. The important state variables and process parameters, i.e., biomass concn., .beta.-galactosidase expression, sucrose consumption, yeast ext. consumption, and specific growth rates of the two cell populations, were evaluated. These variables and parameters along with the differential equations based on material balances as well as the exptl. results obtained were used in a math. model for the fed-batch cultivation. These correctly verified the exptl. data and clearly illustrated the concept behind the success of the fed-batch strategy under yeast ext. starvation.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 6 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2002:239168 CAPLUS <<LOGINID::20100917>>
DN 136:382701
TI Inositol is specifically involved in the sexual program of the fission yeast Schizosaccharomyces pombe
AU Voicu, Pia-Manuela; Poitelea, Marius; Schweingruber, Martin Ernst; Rusu, Mircea
CS Department of Biochemistry, University of Medicine and Pharmacy Iasi, Iasi, 6600, Rom.
SO Archives of Microbiology (2002), 177(3), 251-258 CODEN: AMICCW; ISSN: 0302-8933
PB Springer-Verlag
DT Journal
LA English
AB The fission ***yeast*** Schizosaccharomyces pombe is a natural ***auxotroph*** for inositol and fails to grow in the complete ***absence*** of it. It was previously reported that a small concn. of inositol in the culture medium supports vegetative growth, but not mating and sporulation, and a ten-fold of that concn. also supports mating and sporulation. The purpose of the ***present*** work was to investigate whether a moderate inositol starvation specifically affected events of the sexual program of development. A homothallic culture grown to the stationary phase in medium with a small inositol concn. was sterile but cells in the stationary phase of growth synchronously entered and completed the sexual cycle when inositol was added, without need of previous cell divisions. This suggests the involvement of inositol in a mechanism (or mechanisms) of the sexual program. The events of the program that were affected by inositol starvation were investigated. Commitment to mating and prodn. of pheromone M were shown not to be inositol-dependent. A diploid strain homozygous at the mating-type locus and carrying a pat1-114 temp.-sensitive mutation in homozygous configuration sporulated under inositol starvation at the restrictive temp.; therefore starvation did not directly affect meiosis or sporulation. In contrast, prodn. of pheromone P and the response of cells to pheromones were found to be inositol-dependent. The possibility that inositol or one of its deriv. compds. is involved in pheromone P secretion and in pheromone signal reception is discussed.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)
RE.CNT 22 THERE ARE 22 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 7 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:820790 CAPLUS <<LOGINID::20100917>>
DN 137:16150
TI Development of Saccharomyces cerevisiae as a model pathogen: a system for the genetic identification of gene products required for survival in the mammalian host environment
AU Goldstein, Alan L.; McCusker, John H.
CS Department of Microbiology, Duke University Medical Center, Durham, NC, 27710, USA
SO Genetics (2001), 159(2), 499-513 CODEN: GENTAE; ISSN: 0016-6731
PB Genetics Society of America
DT Journal
LA English
AB Saccharomyces cerevisiae, a close relative of the pathogenic Candida species, is an emerging opportunistic pathogen. An isogenic series of S. cerevisiae strains, derived from a human clin. isolate, were used to examine the role of evolutionarily conserved pathways in fungal survival in a mouse host. As is the case for the corresponding Candida albicans and Cryptococcus neoformans mutants, S. ***cerevisiae*** purine and

pyrimidine ***auxotrophs*** were severely deficient in survival, consistent with there being evolutionary conservation of survival traits. Resistance to the antifungal drug 5-fluorocytosine was not deleterious and appeared to be slightly advantageous in vivo. Of mutants in three amino acid biosynthetic pathways, only leu2 mutants were severely deficient in vivo. Unlike the glyoxylate cycle, respiration was very important for survival; however, the mitochondrial genome made a respiration-independent contribution to survival. Mutants deficient in pseudohyphal formation were ***tested*** in vivo; flo11.DELTA. mutants were phenotypically neutral while flo8.DELTA., tec1.DELTA., and flo8.DELTA. tec1.DELTA. mutants were slightly deficient. Because of its ease of genetic manipulation and the immense S. cerevisiae database, which includes the best annotated eukaryotic genome sequence, S. cerevisiae is a superb model system for the identification of gene products important for fungal survival in the mammalian host environment.
OSC.G 39 THERE ARE 39 CAPLUS RECORDS THAT CITE THIS RECORD (39 CITINGS)
RE.CNT 84 THERE ARE 84 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 8 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:763228 CAPLUS <<LOGINID::20100917>>
DN 135:314428
TI Positive selection of transformants by auxotroph complementation with enzymatic precursor conversion
IN Silva, Christopher J.
PA Cubist Pharmaceuticals, Inc., USA
SO PCT Int. Appl., 51 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 2001077366 A1 20011018 WO 2001-US11567 20010410 W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
PRAI US 2000-195911P P 20000410
AB This invention relates to a pos. selection method, compds. useful for the pos. selection and appropriate hosts. The method permits one to select a host, or auxotroph, which may be a prokaryote or an eukaryote, based on the ability of the host to express an enzyme(s) capable of catalyzing a reaction that converts a precursor mol. into a mol. or factor necessary for the host's survival. This invention encompasses methods useful to find new enzymes expressing a desired activity, methods of selecting host cells, methods of maintaining a plasmid within a host that do not utilize antibiotics, and methods of expressing proteins or other materials for com. prodn. purposes.
RE.CNT 5 THERE ARE 5 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 9 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:689021 CAPLUS <<LOGINID::20100917>>
DN 136:289572
TI Differences in HAC1 mRNA Processing and Translation between Yeast and Mammalian Cells Indicate Divergence of the Eukaryotic ER Stress Response
AU Bowring, Claire E.; Llewellyn, David H.
CS Department of Medical Biochemistry, University of Wales College of Medicine, Cardiff, Wales, CF14 4XN, UK
SO Biochemical and Biophysical Research Communications (2001), 287(3), 789-800 CODEN: BBRCA9; ISSN: 0006-291X
PB Academic Press
DT Journal
LA English
AB Perturbation of normal endoplasmic reticulum (ER) function induces a stress response found throughout eukaryotes, sometimes termed the unfolded protein response (UPR). In ***yeast*** , ***auxotrophic*** mutants have identified two genes, IRE1 and HAC1, whose products are key components. Normally HAC1 mRNA is not translated owing to a 252-nt intron. Disruption of ER function activates Ire1p to remove this intron through endogenous endoribonuclease activity. Together with tRNA ligase, cleavage and splicing produces a translatable HAC1 mRNA to give Hac1p, a transcription factor that upregulates the expression of genes responsive to ER stress. No Hac1p homolog has been identified in mammalian cells, but Ire1p homologues exist with endoribonuclease activity required for a fully functional UPR, raising the possibility that the key features of the yeast UPR might be conserved in higher eukaryotic cells. To address this, we expressed yeast HAC1 in HeLa and HEK 293T human cell lines, both on its own and as fusions with yellow fluorescent protein (YFP) to investigate its processing and translation. HAC1 mRNA was not processed, but efficiently translated irresp. of whether the cells were subjected to ER stress. Expression of exogenous HAC1 mRNA constructs in yeast showed UPR-induced splicing required the ***presence*** of its 3' UTR. These results suggest that the mammalian ER stress response has diverged from the yeast UPR. (c) 2001 Academic Press.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 10 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:660814 CAPLUS <<LOGINID::20100917>>
DN 136:289655
TI Genetic characterization of the nonconventional yeast hansenula anomala
AU Naumov, Gennadi I.; Naumova, Elena S.; Schuurer, Johan
CS State Institute for Genetics and Selection of Industrial Microorganisms, Moscow, 113545, Russia
SO Research in Microbiology (2001), 152(6), 551-562 CODEN: RMICREW; ISSN: 0923-2508
PB Editions Scientifiques et Medicales Elsevier
DT Journal
LA English
AB We describe genetic, mol. and taxonomic characteristics of the yeast Hansenula anomala. Pulsed-field gel electrophoresis of chromosomal DNAs from 19 H. anomala strains and related species indicated that H. anomala had a clearly different karyotype. Chromosome length polymorphism of the H. anomala strains was independent of their geog. origin and source of isolation. The strains were classified into four groups of similar karyotypes and one strain showed a unique profile. The sizes of chromosomes ranged from 850 to 3500 kb in different strains. The haploid chromosome no. of H. anomala is at least nine. We

have found RAPD primers discriminating at both the species and strain levels. All the primers ***tested*** except the M13 core sequence generated unique patterns with most strains. The results indicate the usefulness of PCR anal. with primer M13 for identification of the H. anomala species. Screening of the CBS (Utrecht) collection strains of H. anomala showed that they are rather difficult objects for genetic hybridization anal. The strains have low fertility, viz. very poor sporulation, low mating type activities and, as a rule, nonviable ascospores. The majority of the hybrids obtained are polyploid, probably tetraploid, as judged by the segregation of control auxotrophic markers. Nevertheless, some monosporic cultures of the strains studied, including the biocontrol ***yeast*** J121, formed diploid hybrids with regular meiotic segregation of control ***auxotrophic*** markers. As a rule, H. anomala isolates are homothallic, showing delayed self-diploidization. Rare stable heterothallic strains of H. anomala also occur.
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 11 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:621409 CAPLUS <<LOGINID::20100917>>
DN 135:369018
TI The centromere-binding factor Cbf1p from Candida albicans complements the methionine ***auxotrophic*** phenotype of ***Saccharomyces*** ***cerevisiae***
AU Eck, Raimund; Stoyan, Tanja; Kunkel, Waldemar
CS Department of Infection Biology, Hans-Knoll-Institute for Natural Products Research, Jena, D-07745, Germany
SO Yeast (2001), 18(11), 1047-1052 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB A gene encoding the centromere binding factor 1 (Cbf1p) of the human pathogenic yeast Candida albicans was cloned and characterized. An open reading-frame was detected which encoded a 223-amino acid protein with a calcd. mol. wt. of 25.8 kDa and a relative isoelec. point of 5.55. It shares 39% overall amino acid sequence identity with Saccharomyces cerevisiae Cbf1p. The CaCBF1 gene was localized on chromosome 4. Southern anal. indicated that CaCBF1 is probably ***present*** as a single copy gene per haploid genome. The CaCBF1 gene under the control of its own promoter was able to complement the methionine auxotrophic growth, the increased mitotic instability of CEN plasmids, and the slow growth of a S. cerevisiae cbf1.DELTA. mutant strain.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)
RE.CNT 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 12 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:616813 CAPLUS <<LOGINID::20100917>>
DN 136:211629
TI Insertional mutagenesis in the n-alkane-assimilating yeast Yarrowia lipolytica: generation of tagged mutations in genes involved in hydrophobic substrate utilization
AU Mauersberger, Stephan; Wang, Hui-Jie; Gaillardin, Claude; Barth, Gerold; Nicaud, Jean-Marc
CS Institut fur Mikrobiologie, Technische Universitat Dresden, Dresden, D-01062, Germany
SO Journal of Bacteriology (2001), 183(17), 5102-5109 CODEN: JOBAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
AB Tagged mutants affected in the degrdn. of hydrophobic compds. (HC) were generated by insertion of a zeta-URA3 mutagenesis cassette (MTC) into the genome of a zeta-free and ura3 deletion-contg. strain of Yarrowia lipolytica. MTC integration occurred predominantly at random by nonhomologous recombination. A total of 8,600 Ura+ transformants were ***tested*** by replica plating for (i) growth on minimal media with alkanes of different chain lengths (decane, dodecane, and hexadecane), oleic acid, tributyrin, or ethanol as the C source and (ii) colonial defects on different glucose-contg. media (YPD, YNBD, and YNBcas). A total of 257 mutants were obtained, of which about 70 were affected in HC degrdn., representing different types of non-alkane-utilizing (Alk-) mutants (phenotypic classes alkA to alkE) and tributyrin degrdn. mutants. Among Alk- mutants, growth defects depending on the alkane chain length were obsd. (alkAa to alkAc). Furthermore, mutants defective in ***yeast*** -hypha transition and ethanol utilization and selected ***auxotrophic*** mutants were isolated. Flanking borders of the integrated MTC were sequenced to identify the disrupted genes. Sequence anal. indicated that the MTC was integrated in the LEU1 locus in N083, a leucine-auxotrophic mutant, in the isocitrate dehydrogenase gene of N156 (alkE leaky), in the thioredoxin reductase gene in N040 (alkAc), and in a peroxine gene (PEX14) in N078 (alkD). This indicates that MTC integration is a powerful tool for generating and analyzing tagged mutants in Y. lipolytica.
OSC.G 33 THERE ARE 33 CAPLUS RECORDS THAT CITE THIS RECORD (33 CITINGS)
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 13 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:520743 CAPLUS <<LOGINID::20100917>>
DN 136:196818
TI A genetic screen for ethanolamine ***auxotrophs*** in ***Saccharomyces*** ***cerevisiae*** identifies a novel mutation in Mcd4p, a protein implicated in glycosylphosphatidylinositol anchor synthesis
AU Storey, M. K.; Wu, W.-I.; Voelker, D. R.
CS Program in Cell Biology, Department of Medicine, National Jewish Medical and Research Center, Denver, CO, 80206, USA
SO Biochimica et Biophysica Acta, Molecular and Cell Biology of Lipids (2001), 1532(3), 234-247 CODEN: BBMLFG; ISSN: 1388-1981
PB Elsevier B.V.
DT Journal
LA English
AB A genetic screen for ethanolamine auxotrophs has identified a novel mutant allele of the morphogenesis checkpoint dependent (MCD)-4 gene, designated mcd4-P301L. In the ***presence*** of a null allele for the phosphatidylserine (PtdSer) decarboxylase 1 gene (psd1.DELTA.), the mcd4-P301L mutation confers temp. sensitivity for growth on minimal medium. This growth defect is reversed by either ethanolamine or choline supplementation. Incubation of mutant cells with [3H]serine followed by anal. of the aminoglycerophospholipids demonstrated a 60% decrease in phosphatidylethanolamine

(PtdEtn) formation compared to parental cells. Chem. anal. of phospholipid content after culture under non-permissive conditions also demonstrated a 60% decrease in the PtdEtn pool compared to the parental strain. Although the morphogenesis checkpoint dependent (MCD)-4 gene and its homologues have been shown to play a role in glycosylphosphatidylinositol (GPI) anchor synthesis, the mcd4-P301L strain displayed normal incorporation of [3H]inositol into both proteins and lipids. Thus, a defect in GPI anchor synthesis does not explain either the ethanolamine auxotrophy or biochem. phenotype of this mutant. We also examd. the growth characteristics and PtdSer metab. of a previously described mcd4-174 mutant strain, with defects in GPI anchor synthesis, protein modification and cell wall maintenance. The mcd4-174, psd1.DELTA. strain is a temp. sensitive ethanolamine auxotroph that requires osmotic support for growth, and displays normal PtdEtn formation compared to parental cells. These results reveal important genetic interactions between PSD1 and MCD4 genes, and provide evidence that Mcd4p can modulate aminoglycerophospholipid metab., in a way independent of its role in GPI anchor synthesis.
OSC.G 15 THERE ARE 15 CAPLUS RECORDS THAT CITE THIS RECORD (15 CITINGS)
RE.CNT 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 14 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:407671 CAPLUS <<LOGINID::20100917>>
DN 135:134392
TI Vacuolar morphology and cell cycle distribution are modified by leucine limitation in ***auxotrophic*** ***Saccharomyces*** ***cerevisiae***
AU Cakar, Z. Petek; Sauer, Uwe; Bailey, James E.; Muller, Martin; Stolz, Martin; Wallimann, Theo; Schlattner, Uwe
CS Institute of Biotechnology, ETH Zurich, Zurich, 8093, Switz.
SO Biology of the Cell (2000), 92(8/9), 629-637 CODEN: BCELDF; ISSN: 0248-4900
PB Editions Scientifiques et Medicales Elsevier
DT Journal
LA English
AB Yeast vacuoles are highly dynamic and flexible organelles. The authors have previously shown that subtle, often unrecognized amino acid limitations lead to much lower final cell densities in cultures of different commonly used ***auxotrophic*** ***Saccharomyces*** ***cerevisiae*** strains. Here, they demonstrate for two of these strains, CEN.PK 113.6B and CBS7752, that such subtle leucine limitations also affect the no. and morphol. of vacuoles, and that these changes are correlated with the cell cycle in batch cultures in a similar way as is known from synchronized cultures. Morphol. aspects were studied by electron microscopy, using advanced high pressure freezing/freeze-substitution techniques for sample prepn. that so far have been barely successful in yeast. Cells of leucine-limited cultures had single, large vacuoles with a hexagonal tonoplast pattern and were partially arrested in G1 phase. To relieve leucine-limitation, addnl. leucine was supplied extracellularly via the medium or intracellularly via enhanced leucine biosynthesis due to plasmid-based expression of a leucine marker gene. Such cultures reached more than two-fold higher final optical densities in stationary phase. Cells in later growth phase were characterized by fragmented vacuoles lacking any tonoplast pattern and by a smaller proportion of cells in G1 phase. These drastic effects of subtle leucine limitation on cell physiol., vacuolar morphol. and cell cycle distribution ***present*** a note of caution for morphol. and cell cycle studies in yeast.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)
RE.CNT 36 THERE ARE 36 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 15 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:241335 CAPLUS <<LOGINID::20100917>>
DN 135:43402
TI Anaerobiosis induces complex changes in sterol esterification pattern in the yeast Saccharomyces cerevisiae
AU Valachovic, M.; Hronska, L.; Hapala, I.
CS Institute of Animal Biochemistry and Genetics, Slovak Academy of Sciences, Ivanka pri Dunaji, 900 28, Slovakia
SO FEMS Microbiology Letters (2001), 197(1), 41-45 CODEN: FMLED7; ISSN: 0378-1097
PB Elsevier Science B.V.
DT Journal
LA English
AB ***Yeast*** ***Saccharomyces*** ***cerevisiae*** is ***auxotrophic*** for ergosterol in the ***absence*** of oxygen. We showed that complex changes in esterification of exogenously supplied sterols were also induced by anaerobiosis. Utilization of oleic acid for sterol esterification was significantly impaired in anaerobic cells. Furthermore, anaerobic cells fed different sterols exhibited striking variation in esterification efficiency (high levels of sterol esters for cholesterol and sitosterol, low levels for ergosterol, lanosterol or stigmasterol). Relative activities of two yeast acyl-CoA:sterol acyltransferases (Are1p and Are2p) changed in response to anaerobiosis: while Are2p was dominant under aerobic conditions, Are1p provided the major activity in the ***absence*** of oxygen. Our results indicate that sterol esters may fulfil different roles in aerobic and anaerobic cells.
OSC.G 15 THERE ARE 15 CAPLUS RECORDS THAT CITE THIS RECORD (15 CITINGS)
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 16 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:206647 CAPLUS <<LOGINID::20100917>>
DN 134:350453
TI A genetic investigation of the essential role of glutathione. Mutations in the proline biosynthesis pathway are the only suppressors of glutathione ***auxotrophy*** in ***yeast***
AU Spector, Daniel; Labarre, Jean; Toledano, Michel B.
CS Service de Biochimie et Genetique Moleculaire, Commissariat a l'Energie Atomique, Gif-sur-Yvette, F-91191, Fr.
SO Journal of Biological Chemistry (2001), 276(10), 7011-7016 CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB In an attempt to elucidate the essential function of GSH in ***Saccharomyces*** ***cerevisiae*** , suppressors of the GSH ***auxotrophy*** of .DELTA.gsh1, a strain lacking the rate-limiting enzyme of GSH biosynthesis, were sought. Specific mutations of PRO2, the 2nd enzyme in proline biosynthesis, permitted the growth of .DELTA.gsh1 in the ***absence*** of exogenous GSH. The suppression mechanism by alleles of PRO2

involved the biosynthesis of a trace amt. of GSH. Deletion of PRO1, the 1st enzyme of the proline biosynthesis pathway, or PRO2 eliminated the suppression, suggesting that .gamma.-glutamyl phosphate, the product of Pro1 and the physiol. substrate of Pro2, is required as an obligate substrate of suppressor alleles of PRO2 for GSH synthesis. A mutagenesis of a .DELTA.gsh1 strain also lacking the proline pathway failed to generate any suppressor mutants under either aerobic or anaerobic conditions, confirming that GSH is essential in yeast. This essential function is not related to DNA synthesis based on the terminal phenotype of GSH-depleted cells or to toxic accumulation of non-native protein disulfides. Anal. of the suppressor strain demonstrates that normal GSH levels are required for the tolerance to oxidants under acute, but not chronic stress conditions.
OSC.G 29 THERE ARE 29 CAPLUS RECORDS THAT CITE THIS RECORD (29 CITINGS)
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 17 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:126046 CAPLUS <<LOGINID::20100917>>
DN 134:323244
TI A novel gene conserved from yeast to humans is involved in sterol biosynthesis
AU Gachotte, D.; Eckstein, J.; Barbuch, R.; Hughes, T.; Roberts, C.; Bard, M.
CS Department of Biology, Indiana University-Purdue University Indianapolis, Indianapolis, IN, 46202, USA
SO Journal of Lipid Research (2001), 42(1), 150-154 CODEN: JLPRAW; ISSN: 0022-2275
PB Lipid Research, Inc.
DT Journal
LA English
AB The ERG28 gene was originally identified by microarray expression profiling as possibly involved in the Saccharomyces cerevisiae sterol pathway. Microarray analyses suggested that the transcription pattern of ERG28 closely followed that of genes involved in sterol synthesis. ERG28 was also found in Schizosaccharomyces pombe and Arabidopsis as well as humans, and in the latter was shown to be highly expressed in adult ***testis*** tissue. All four proteins contain potential transmembrane domain(s). Gas chromatog.-mass spectrometry anal. of an ERG28-deleted S. ***cerevisiae*** strain (which is slow growing but not ***auxotrophic*** for ergosterol) indicates a lesion in sterol C-4 demethylation. Sterol profiles indicate accumulation of 3-keto and carboxylic acid sterol intermediates, which are involved in removing the two C-4 Me groups from the sterol A ring. Similar intermediates have previously been demonstrated to accumulate in erg26 (sterol dehydrogenase/decarboxylase) and erg27 (3-ketoreductase) mutants in yeast. We speculate that the role of the Erg28 protein (Erg28p) may be either to tether Erg26p and Erg27p to the endoplasmic reticulum or to facilitate interaction between these proteins.
OSC.G 35 THERE ARE 35 CAPLUS RECORDS THAT CITE THIS RECORD (35 CITINGS)
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 18 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2001:92889 CAPLUS <<LOGINID::20100917>>
DN 135:207961
TI Adaptive reversions of a frameshift mutation in arrested Saccharomyces cerevisiae cells by simple deletions in mononucleotide repeats
AU Heidenreich, E.; Wintersberger, U.
CS Division of Molecular Genetics, Institute of Cancer Research, University of Vienna, Vienna, A-1090, Austria
SO Mutation Research, Fundamental and Molecular Mechanisms of Mutagenesis (2001), 473(1), 101-107 CODEN: MUREAV; ISSN: 0027-5107
PB Elsevier Science B.V.
DT Journal
LA English
AB Adaptive mutations are characterized as the outcome of an as yet unknown mechanism, which allows a few individuals of a cell population to overcome a starvation-induced cell cycle arrest and to proliferate. A release from such a non-lethal growth limitation is accomplished by mutations generated without DNA replication. Originally adaptive mutations were described in Escherichia coli, but more recently also in a simple eukaryote, the budding yeast Saccharomyces cerevisiae. We are studying the adaptive reversion of a frameshift allele which occurs when an ***auxotrophic*** ***yeast*** strain is starved for the amino acid essential for its proliferation. In this communication, we report on the DNA sequences from the locus concerned. Comparison between sequences from revertant clones which arose several days after growth arrest by starvation and those from revertants produced during proliferation shows significantly different mutation spectra: for replication-dependent revertants nucleotide gains and losses in a variety of sequence contexts are reasonably balanced, whereas for the replication-independent, i.e. adaptive, revertants mainly simple deletions in mononucleotide repeats were obsd. These mutations resemble those known to originate from DNA polymerase slippage errors which were miscorrected or had escaped correction by the mismatch repair machinery. Our data ***present*** strong evidence for differences in the mechanistic origins of adaptive vs. DNA replication-dependent mutations in a eukaryote. Most probably, mutations in non-replicating cells contribute to evolution, and if conserved in mammals, to human carcinogenesis.
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 19 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:875313 CAPLUS <<LOGINID::20100917>>
DN 134:251277
TI Two-stage cultivation of recombinant Saccharomyces cerevisiae to enhance plasmid stability under non-selective conditions: experimental study and modeling
AU Gupta, J. C.; Pandey, G.; Mukherjee, K. J.
CS Centre for Biotechnology, Jawaharlal Nehru University, New Delhi, 110 067, India
SO Enzyme and Microbial Technology (2001), 28(1), 89-99 CODEN: EMTED2; ISSN: 0141-0229
PB Elsevier Science Ireland Ltd.
DT Journal
LA English
AB A leucine ***auxotroph*** strain of ***Saccharomyces*** ***cerevisiae*** was used to study plasmid stability and expression using a recombinant plasmid, which contained a foreign gene for firefly luciferase (luc). This

recombinant yeast was ***tested*** in a series of continuous cultures in semi-defined media with varying concns. of yeast ext. in order to study its effect on stability. While the biomass concn. and luciferase activity increased with increasing concns. of yeast ext., the plasmid stability declined. An anal. of the growth rates showed that the recombinants enjoyed a growth rate advantage over the plasmid-free cells at critically low yeast ext. concns., possibly due to leucine starvation in the media. A two-stage cultivation strategy was designed in order to create a yeast ext. limited environment so that plasmid-free cells could not grow and overtake the recombinant cells. The cells were cultivated in selective media in the first stage, and then transferred continuously to the second stage where the media was enriched by feeding yeast ext. The feed rate was kept low in order to ensure yeast ext. and hence leucine starvation, thereby selecting against the plasmid-free cells. This strategy resulted in a stable existence of recombinant cells, which stabilized around 60% at steady state during the ***tested*** period of cultivation. The complex nitrogen feed helped in increasing the cell d. and volumetric activity by .apprx.9 and 18-fold resp. with respect to that achieved in minimal medium. The exptl. data was used to formulate a math. model to predict cell growth and plasmid stability in two-stage cultivation, which correctly explained the exptl. data.
OSC.G 14 THERE ARE 14 CAPLUS RECORDS THAT CITE THIS RECORD (14 CITINGS)
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 20 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:525494 CAPLUS <<LOGINID::20100917>>
DN 133:249480
TI Murine FATP alleviates growth and biochemical deficiencies of yeast fat1.DELTA. strains
AU DiRusso, Concetta C.; Connell, Elise J.; Faergeman, Nils J.; Knudsen, Jens; Hansen, Jan K.; Black, Paul N.
CS Center for Cardiovascular Sciences, Albany Medical College, Albany, NY, 12208-3479, USA
SO European Journal of Biochemistry (2000), 267(14), 4422-4433 CODEN: EJBCAI; ISSN: 0014-2956
PB Blackwell Science Ltd.
DT Journal
LA English
AB Saccharomyces cerevisiae is an ideal model eukaryote for studying fatty-acid transport. ***Yeast*** are ***auxotrophic*** for unsatd. fatty acids when grown under hypoxic conditions or when the fatty-acid synthase inhibitor cerulenin is included in the growth media. The FAT1 gene encodes a protein, Fat1p, which is required for maximal levels of fatty-acid import and has an acyl CoA synthetase activity specific for very-long-chain fatty acids suggesting this protein plays a pivotal role in fatty-acid trafficking. In the ***present*** work, the authors ***present*** evidence that Fat1p and the murine fatty-acid transport protein (FATP) are functional homologs. FAT1 is essential for growth under hypoxic conditions and when cerulenin was included in the culture media in the ***presence*** or ***absence*** of unsatd. fatty acids. FAT1 disruptants (fat1.DELTA.) fail to accumulate the fluorescent long-chain fatty acid fatty-acid analog 4,4-difluoro-5-methyl-4-bora-3a,4a-diaza-s-indacene-3-dodecanoic acid (C1-BODIPY-C12), have a greatly diminished capacity to transport exogenous long-chain fatty acids, and have very long-chain acyl CoA synthetase activities that were 40% wild-type. The depression in very long-chain acyl CoA synthetase activities were not apparent in cells grown in the ***presence*** of oleate. Addnl., .beta.-oxidn. of exogenous long-chain fatty acids is depressed to 30% wild-type levels. The redn. of .beta.-oxidn. was correlated with a depression of intracellular oleoyl CoA levels in the fat1.DELTA. strain following incubation of the cells with exogenous oleate. Expression of either Fat1p or murine FATP from a plasmid in a fat1.DELTA. strain restored these phenotypic and biochem. deficiencies. Fat1p and FATP restored growth of fat1.DELTA. cells in the ***presence*** of cerulenin and under hypoxic conditions. Furthermore, fatty-acid transport was restored and was found to be chain length specific: octanoate, a medium-chain fatty acid was transported in a Fat1p- and FATP-independent manner while the long-chain fatty acids myristate, palmitate, and oleate required either Fat1p or FATP for maximal levels of transport. Lignoceryl CoA synthetase activities were restored to wild-type levels in fat1.DELTA. strains expressing either Fat1p or FATP. Fat1p or FATP also restored wild-type levels of .beta.-oxidn. of exogenous long-chain fatty acids. These data show that Fat1p and FATP are functionally equiv. when expressed in yeast and play a central role in fatty-acid trafficking.
OSC.G 34 THERE ARE 34 CAPLUS RECORDS THAT CITE THIS RECORD (34 CITINGS)
RE.CNT 44 THERE ARE 44 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 21 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:291241 CAPLUS <<LOGINID::20100917>>
DN 133:234961
TI A counterselection for the tryptophan pathway in yeast: 5-fluoroanthranilic acid resistance
AU Toyn, Jeremy H.; Gunyuzlu, Paul L.; White, W. Hunter; Thompson, Lorin A.; Hollis, Gregory F.
CS Department of Applied Biotechnology, DuPont Pharmaceuticals Co., Wilmington, DE, 19880, USA
SO Yeast (2000), 16(6), 553-560 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB The ability to counterselect, as well as to select for, a genetic marker has numerous applications in microbial genetics. Described here is the use of 5-fluoroanthranilic acid for the counterselection of TRP1, a commonly used genetic marker in the yeast Saccharomyces cerevisiae. Counterselection using 5-fluoroanthranilic acid involves antimetabolism by the enzymes of the tryptophan biosynthetic pathway, such that trp1, trp3, trp4 or trp5 strains, which lack enzymes required for the conversion of anthranilic acid to tryptophan, are resistant to 5-fluoroanthranilic acid. Commonly used genetic procedures, such as selection for loss of a chromosomally integrated plasmid, and a replica-plating method to rapidly assess genetic linkage in self-replicating shuttle vectors, can now be carried out using the TRP1 marker gene. In addn., novel tryptophan auxotrophs can be selected using 5-fluoroanthranilic acid.
OSC.G 32 THERE ARE 32 CAPLUS RECORDS THAT CITE THIS RECORD (32 CITINGS)
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 22 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 2000:248069 CAPLUS <<LOGINID::20100917>>
DN 133:42188

TI Production of 5-aminolevulinic acid by a mutant strain of a photosynthetic bacterium - monograph
AU Kamiyama, Hiroki; Hotta, Yasushi; Tanaka, Tohru; Nishikawa, Seiji; Sasaki, Ken
CS R&D Promotion Dep., Cosmo Res. Inst., Tokyo, 108-8564, Japan
SO Seibutsu Kogaku Kaishi (2000), 78(2), 48-55 CODEN: SEKAEA; ISSN: 0919-3758
PB Nippon Seibutsu Kogakkai
DT Journal; General Review
LA Japanese
AB A review with 32 refs. The photosynthetic bacterium Rhodobacter spheroides accumulates 5-aminolevulinic acid (ALA), a precursor in tetrapyrrole biosynthesis, under light illumination and upon addn. of levulinic acid as an inhibitor of ALA dehydratase. To generate an industrial strain that produces ALA in the ***absence*** of light, we sequentially mutated R. spheroides using N-methyl-N'-nitro-N-nitrosoguanidine (NTG). The mutant strain CR-286 was isolated as an ALA producer in the ***presence*** of ***yeast*** ext. using low-melting-point agarose gel contg. the ALA ***auxotroph*** Escherichia coli. Subsequent mutant strains were screened by cultivation in the ***absence*** of light and assayed for ALA by the Ehrlich reaction in a 96-well microtiter plate. The strain CR-386, derived from R. spheroides CR-286, was selected as a mutant that exhibited significant ALA accumulation. While CR-286 required light illumination for ALA prodn., CR-386 was able to accumulate 1.5 mM ALA in the ***presence*** of glucose, glycine, levulinic acid, and yeast ext. with agitation in the ***absence*** of light. Another strain, CR-450, derived from CR-386, was further selected as a mutant that exhibited significant ALA accumulation but no accumulation of aminoacetone, an analog of ALA. CR-450 accumulated 3.8 mM ALA under the same conditions. Similarly, the mutant strain CR-520, derived from CR-450, and CR-606, derived from CR-520, accumulated 8.1 mM and 11.2 mM ALA, resp. In batch fermn., strain CR-606 accumulated 20 mM ALA over 18 h after the addn. of glycine, levulinic acid, glucose, and yeast ext. Finally, the strain CR-720, derived from CR-606, was selected as a mutant that was stable and superior to strain CR-606 in ALA accumulation.
OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)

L17 ANSWER 23 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:793449 CAPLUS <<LOGINID::20100917>>
DN 132:218729
TI The FAD binding sites of human liver monoamine oxidases A and B: investigation of the role of flavin ribityl side chain hydroxyl groups in the covalent flavinylation reaction and catalytic activities
AU Miller, J. R.; Guan, N.; Hubalek, F.; Edmondson, D. E.
CS Department of Biochemistry, Rollins Research Center, Emory University School of Medicine, Atlanta, GA, USA
SO Biochimica et Biophysica Acta, Protein Structure and Molecular Enzymology (2000), 1476(1), 27-32 CODEN: BBAEDZ; ISSN: 0167-4838
PB Elsevier B.V.
DT Journal
LA English
AB The role of ribityl side chain hydroxyl groups of the flavin moiety in the covalent flavinylation reaction and catalytic activities of recombinant human liver monoamine oxidases (MAO) A and B have been investigated using the riboflavin analog: N(10)-.omega.-hydroxypentyl-isoalloxazine. Using a rib5 disrupted strain of ***Saccharomyces*** ***cerevisiae*** which is ***auxotrophic*** for riboflavin, MAO A and MAO B were expressed sep. under control of a galactose inducible GAL10/CYC1 promoter in the ***presence*** of N(10)-.omega.-hydroxypentyl-isoalloxazine as the only available riboflavin analog. Anal. of mitochondrial membrane proteins shows both enzymes to be expressed at levels comparable to those cultures grown on riboflavin and to contain covalently bound flavin. Catalytic activities, as monitored by kynuramine oxidn., are equiv. to (MAO A) or 2-fold greater (MAO B) than control prepns. expressed in the ***presence*** of riboflavin. Although N(10)-.omega.-hydroxypentyl-isoalloxazine is unable to support growth of riboflavin ***auxotrophic*** S. ***cerevisiae*** , it is converted to the FMN level by ***yeast*** cell free exts. The FMN form of the analog is converted to the FAD level by the yeast FAD synthetase, as shown by expression of the recombinant enzyme in Escherichia coli. These data show that the ribityl hydroxyl groups of the FAD moiety are not required for covalent flavinylation or catalytic activities of monoamine oxidases A and B. This is in contrast to the suggestion based on mutagenesis studies that an interaction between the 3'-hydroxyl group of the flavin and the .beta.-carbonyl of Asp227 is required for the covalent flavinylation reaction of MAO B.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)
RE.CNT 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 24 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:569595 CAPLUS <<LOGINID::20100917>>
DN 132:33063
TI The N-end rule pathway is required for import of histidine in yeast lacking the kinesin-like protein Cin8p
AU Xie, Youming; Varshavsky, Alexander
CS Division of Biology, Caltech, Pasadena, CA, 91125, USA
SO Current Genetics (1999), 36(3), 113-123 CODEN: CUGED5; ISSN: 0172-8083
PB Springer-Verlag
DT Journal
LA English
AB The N-end rule pathway is a ubiquitin-dependent proteolytic system whose targets include proteins bearing destabilizing N-terminal residues. The authors carried out a synthetic lethal screen for Saccharomyces cerevisiae mutants that require the N-end rule pathway for cell viability. A mutant thus identified, termed sln2, could not grow in the ***absence*** of Ubr1p, the recognition component of the N-end rule pathway, which was not essential for viability of the parental strain under the same conditions. Further anal. showed that inviability of sln2ubr1.DELTA. cells could be rescued either by the HIS3 gene (which was ***absent*** from the parental strain) or by a high concn. of histidine in the medium. This defect in histidine uptake, exhibited by the sln2 mutant in the ***absence*** but not in the ***presence*** of Ubr1p, was traced to the gene HIP1, which encodes the histidine transporter. HIP1 was underexpressed in sln2 ubr1.DELTA. cells, in comparison to either sln2 UBR1 or SLN2 ubr1.DELTA. cells. Yet another property of the sln2 mutant was its inviability at 37.degree., which could not be rescued by either UBR1 or HIS3. This feature of sln2 allowed the cloning of SLN2, which was a gene called CIN8, encoding a kinesin-like protein. Thus, either the N-end rule pathway or Cin8p must be ***present*** for the viability-sustaining rate of histidine import in S. ***cerevisiae*** ***auxotrophic***

for histidine. The authors consider possible mechanisms of this previously unsuspected link between kinesins, ubiquitin-dependent proteolysis, and the import of histidine.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 61 THERE ARE 61 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 25 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:554610 CAPLUS <<LOGINID::20100917>>
DN 131:283826
TI Control of filament formation in Candida albicans by polyamine levels
AU Herrero, Ana B.; Lopez, M. Carmen; Garcia, Susana; Schmidt, Axel; Spaltmann, Frank; Ruiz-Herrera, Jose; Dominguez, Angel
CS Departamento de Microbiologia y Genetica, IMB/CSIC, Universidad de Salamanca, Salamanca, 37007, Spain
SO Infection and Immunity (1999), 67(9), 4870-4878 CODEN: INFIBR; ISSN: 0019-9567
PB American Society for Microbiology
DT Journal
LA English
AB Candida albicans, the most common fungal pathogen, regulates its cellular morphol. in response to environmental conditions. The ODC gene, which encodes ornithine decarboxylase, a key enzyme in polyamine biosynthesis, was isolated and disrupted. Homozygous null Candida mutants behaved as polyamine ***auxotrophs*** and grew exclusively in the ***yeast*** form at low polyamine levels (0.01 mM putrescine) under all conditions ***tested*** . An increase in the polyamine concn. (10 mM putrescine) restored the capacity to switch from the yeast to the filamentous form. The strain with a deletion mutation also showed increased sensitivity to salts and calcofluor white. This Candida odc/odc mutant was virulent in a mouse model. The results suggest a model in which polyamine levels exert a pleiotrophic effect on transcriptional activity.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)
RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 26 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:536344 CAPLUS <<LOGINID::20100917>>
DN 131:269395
TI Restoration of inositol prototrophy in the fission yeast Schizosaccharomyces pombe
AU Ingavale, Susham S.; Bachhawat, Anand K.
CS Institute of Microbial Technology, Chandigarh, 160036, India
SO Microbiology (Reading, United Kingdom) (1999), 145(8), 1903-1910 CODEN: MROBEO; ISSN: 1350-0872
PB Society for General Microbiology
DT Journal
LA English
AB The biosynthesis of inositol requires only two enzymes, inositol-1-phosphate synthase (encoded by INO1) and an inositol monophosphatase, but the regulation of inositol biosynthesis is under multiple controls and is exquisitely regulated. In the budding yeast Saccharomyces ***cerevisiae*** , mutations in any of 26 different genes lead to inositol ***auxotrophy*** . The fission ***yeast*** Schizosaccharomyces pombe, however, is a natural inositol ***auxotroph*** . An investigation has been initiated to examine the possible reasons that might have led to inositol auxotrophy in Sch. pombe. Complementation with a genomic library of an inositol prototrophic yeast indicated that a Pichia pastoris INO1 gene alone could confer inositol prototrophy to Sch. pombe and that the gene was ***absent*** in Sch. pombe. To investigate possible reasons for the loss of INO1 gene in Sch. pombe, an attempt was made to disrupt inositol homeostasis in Sch. pombe by overprodn. of intracellular inositol, but this did not lead to any discernible adverse effects. The sources of inositol in the natural environment of Sch. pombe were also examd. As the natural environment of Sch. pombe contains significant amts. of phytic acid (inositol hexaphosphate), an investigation was carried out and it was discovered that Sch. pombe can utilize phytic acid as a source of inositol under very specific conditions.
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)
RE.CNT 46 THERE ARE 46 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 27 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:532830 CAPLUS <<LOGINID::20100917>>
DN 131:268097
TI Toxicity of copper, cobalt, and nickel salts is dependent on histidine metabolism in the yeast Saccharomyces cerevisiae
AU Pearce, David A.; Sherman, Fred
CS Department of Biochemistry and Biophysics, University of Rochester School of Medicine and Dentistry, Rochester, NY, 14642, USA
SO Journal of Bacteriology (1999), 181(16), 4774-4779 CODEN: JOBAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
AB The pH-dependent inhibition by 22 metal salts has been systematically investigated for the yeast Saccharomyces cerevisiae. The authors have established that the inhibition of growth by Cu, Co, or Ni salts is markedly enhanced by histidine auxotrophy and by increasing the pH of the medium. Each of the his1-his7 mutant strains were unable to grow in the ***presence*** of elevated levels of Cu, Co, or Ni at nearly neutral pHs, in contrast to His+ strains, which grew under these conditions. The Cu, Co, or Ni inhibition was reversed by the addn. of histidine to the medium. Deletion of the high-affinity histidine permease Hip1p in His- strains resulted in even greater sensitivity to Cu, Co, and Ni and the requirement of an even higher level of histidine to reverse the inhibition. These results suggest that intracellular histidine, most likely in the vacuole, diminishes the pH-dependent toxicity of Cu, Co, and Ni. Furthermore, the toxicity of many salts is exacerbated in strains with a defective vacuolar H+-ATPase, which abolishes the ability of yeast to maintain an acidic vacuole, a compartment known to sequester metal compds. It is suggested that the accumulation of histidine in the vacuole is a normal process used to detoxify Cu, Co, and Ni.
OSC.G 35 THERE ARE 35 CAPLUS RECORDS THAT CITE THIS RECORD (35 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 28 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:531790 CAPLUS <<LOGINID::20100917>>

DN 132:63466
TI Breeding of apple-wine yeast
AU Takahasi, Hitoe; Kimura, Norihisa; Kawano, Ikuo
CS Food Div., Gunma Prefect. Ind. Technol. Res. Lab., Maebashi, 371-0845, Japan
SO Gunma-ken Kogyo Shikenjo Kenkyu Hokoku (1999), Volume Date 1998 73-76 CODEN: GKHOEF; ISSN: 1341-0245
PB Gunma-ken Kogyo Shikenjo
DT Journal
LA Japanese
AB Yeast strains were bred for apple-wine making by protoplast fusion between naturally selected yeasts and a wine yeast. Yeast producing apple-like aromas like isoamyl alc., isoamyl acetate and hexyl acetate were selected from flowers and soil. Of the yeast strains, No. 3 was selected from the aroma profile. The No. 3 was classified as Ascomycotina and showed a multi-budding property. Although No. 3 produced apple-like aromas, the strain showed low fermentability in apple juice. No. 3 (pyridoxine requiring ***auxotroph***) and ***Saccharomyces*** ***cerevisiae*** W-3 (wine ***yeast*** , pantothenic acid requiring ***auxotroph***) were fused under conventional conditions. Of the fusants, 7 fused strains were selected by evaluation of aroma profiles after fermn. ***tests*** . Those 7 strains fermented apple juices as fast as W-3, and produced aromas like isoamyl alc., isoamyl acetate and hexyl acetate. Of the 7 strains, 1-6, 2-7, and 2-24 were selected by sensory evaluation. Although the 3 strains produced apple-wine with a little bitter and astringent taste, these strains seemed to be promising as the apple-wine yeast with further improvement.

L17 ANSWER 29 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:504068 CAPLUS <<LOGINID::20100917>>
DN 131:254851
TI Stress tolerance in a yeast lipid mutant: membrane lipids influence tolerance to heat and ethanol independently of heat shock proteins and trehalose
AU Swan, Tracey M.; Watson, Kenneth
CS School of Biological Sciences, University of New England, Armidale, 2351, Australia
SO Canadian Journal of Microbiology (1999), 45(6), 472-479 CODEN: CJMIAZ; ISSN: 0008-4166
PB National Research Council of Canada
DT Journal
LA English
AB The response of a ***yeast*** unsatd. fatty acid ***auxotroph*** , defective in .DELTA.9-desaturase activity, to heat and ethanol stresses was examd. The most heat- and ethanol-tolerant cells had membranes enriched with oleic acid (C18:1), followed in order by cells enriched with linoleic (C18:2) and linolenic (C18:3) acids. Cells subjected to a heat shock (25-37.degree.C for 30 min) accumulated trehalose and synthesized typical heat shock proteins. Although there were no obvious differences in protein profiles attributable to lipid supplementation of the mutant, relative protein synthesis as detd. by densitometric anal. of autoradiograms suggested that hsp expression was different. However, there was no consistent relationship between the synthesis of heat shock proteins and the acquisition of thermotolerance in the lipid supplemented auxotroph or related wild type. Furthermore, trehalose accumulation was also not closely related to stress tolerance. On the other hand, the data ***presented*** indicated a more consistent role for membrane lipid compn. in stress tolerance than trehalose, heat shock proteins, or ergosterol. The authors suggest that the sensitivity of C18:3-enriched cells to heat and ethanol may be attributable to membrane damage assocd. with increases in membrane fluidity and oxygen-derived free radical attack of membrane lipids.
OSC.G 37 THERE ARE 37 CAPLUS RECORDS THAT CITE THIS RECORD (37 CITINGS)
RE.CNT 60 THERE ARE 60 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 30 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:399467 CAPLUS <<LOGINID::20100917>>
DN 131:180627
TI Cloning and functional expression of a cDNA encoding a metabolic acyl-CoA .DELTA.9-desaturase of the cabbage looper moth, Trichoplusia ni
AU Liu, Weitian; Ma, Peter W. K.; Marsella-Herrick, Patricia; Rosenfield, Claire-Lise; Knipple, Douglas C.; Roelofs, Wendell
CS Department of Entomology, New York State Agricultural Experiment Station, Cornell University, Geneva, NY, 14456, USA
SO Insect Biochemistry and Molecular Biology (1999), 29(5), 435-443 CODEN: IBMBES; ISSN: 0965-1748
PB Elsevier Science Ltd.
DT Journal
LA English
AB Acyl-CoA .DELTA.9-desaturases play essential roles in fatty acid metab. and the regulation of cell membrane fluidity. In this research, a cDNA sequence was obtained from Trichoplusia ni adult fat body mRNA by using RT-PCR with degenerate primers based on other characterized .DELTA.9-desaturase sequences. The remainder of the sequence was amplified using 3'- and 5'-RACE. A 1439 bp cDNA reconstructed from three overlapping PCR products contains an ORF encoding a 353-amino acids (aa) protein that shows clear homol. (greater than 50% aa identity and greater than 65% aa similarity to characterized insect and vertebrate desaturases). The ORF of this cDNA was subcloned into an expression vector, which relieved the unsatd. fatty acid (UFA) ***auxotrophy*** of a desaturase-deficient ***yeast*** strain following genetic transformation. The newly characterized desaturase from T. ni produced fatty acids .DELTA.9-16 and .DELTA.9-18 in a 1:6 ratio, compared to a 5:1 ratio, resp., with the yeast .DELTA.9 desaturase. A Northern blot hybridization and a RT-PCR expt. showed that temporal and tissue-specific patterns of expression of the corresponding mRNA are distinct from those of the .DELTA.11-desaturase mRNA ***present*** in the pheromone glands of adult females. Based on its homol. to other desaturases, the widespread distribution of its corresponding mRNA in various tissues, and its functional assay, the authors conclude that this cDNA encodes the apoprotein corresponding to the desaturase component of the metabolic .DELTA.9-desaturase complex of T. ni.
OSC.G 33 THERE ARE 33 CAPLUS RECORDS THAT CITE THIS RECORD (33 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 31 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:225325 CAPLUS <<LOGINID::20100917>>
DN 131:99082
TI The Arabidopsis HAL2-like gene family includes a novel sodium-sensitive phosphatase
AU Gil-Mascarell, Rosario; Lopez-Coronado, Jose M.; Belles, Jose M.; Serrano, Ramon; Rodriguez, Pedro L.

CS Instituto de Biologia Molecular y Celular de Plantas, Universidad Politecnica de Valencia-Consejo Superior de Investigaciones Cientificas, Valencia, E-46022, Spain
SO Plant Journal (1999), 17(4), 373-383 CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Science Ltd.
DT Journal
LA English
AB The yeast HAL2 gene encodes a lithium- and sodium-sensitive phosphatase that hydrolyzes 3'-phosphoadenosine-5'-phosphate (PAP). Salt toxicity in yeast results from Hal2 inhibition and accumulation of PAP, which inhibits sulfate assimilation and RNA processing. The authors have investigated whether the model plant Arabidopsis thaliana contains sodium-sensitive PAP phosphatases. The Arabidopsis HAL2-like gene family is composed of three members: AtAHL and AtSAL2, characterized in the ***present*** work, and the previously identified AtSAL1. The AtAHL and AtSAL2 cDNAs complement the ***auxotrophy*** for methionine of the ***yeast*** hal2 mutant and the recombinant proteins catalyze the conversion of PAP to AMP in a Mg2+-dependent reaction sensitive to inhibition by Ca2+ and Li+. The PAP phosphatase activity of AtAHL is sensitive to physiol. concns. of Na+, whereas the activities of AtSAL1 and AtSAL2 are not. Another important difference is that AtAHL is very specific for PAP while AtSAL1 and AtSAL2 also act as inositol polyphosphate 1-phosphatases. AtAHL constitutes a novel type of sodium-sensitive PAP phosphatase which could act coordinately with plant sulfotransferases and serve as target of salt toxicity in plants.
OSC.G 34 THERE ARE 34 CAPLUS RECORDS THAT CITE THIS RECORD (34 CITINGS)
RE.CNT 43 THERE ARE 43 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 32 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:200257 CAPLUS <<LOGINID::20100917>>
DN 131:83611
TI Efficient homologous and illegitimate recombination in the opportunistic yeast pathogen Candida glabrata
AU Cormack, Brendan P.; Falkow, Stanley
CS Department of Microbiology and Immunology, Stanford University School of Medicine, Stanford, CA, 94305-5402, USA
SO Genetics (1999), 151(3), 979-987 CODEN: GENTAE; ISSN: 0016-6731
PB Genetics Society of America
DT Journal
LA English
AB The opportunistic pathogen Candida glabrata causes significant disease in humans. To develop genetic tools to investigate the pathogenicity of this organism, we have constructed ura3 and his3 auxotrophic strains by deleting the relevant coding regions in a C. glabrata clin. isolate. Linearized plasmids carrying a ***Saccharomyces*** ***cerevisiae*** URA3 gene efficiently transformed the ura3 ***auxotroph*** to prototrophy. Homologous recombination events were obsd. when the linearized plasmid carried short terminal regions homologous with the chromosome. In contrast, in the ***absence*** of any chromosomal homol., the plasmid integrated by illegitimate recombination into random sites in the genome. Sequence anal. of the target sites revealed that for the majority of illegitimate transformants there was no microhomol. with the integration site. Approx. 0.25% of the insertions resulted in amino acid auxotrophy, suggesting that insertion was random at a gross level. Sequence anal. suggested that illegitimate recombination is nonrandom at the single-gene level and that the integrating plasmid has a preference for inserting into noncoding regions of the genome. Anal. of the relative nos. of homologous and illegitimate recombination events suggests that C. glabrata possesses efficient systems for both homologous and nonhomologous recombination.
OSC.G 48 THERE ARE 48 CAPLUS RECORDS THAT CITE THIS RECORD (48 CITINGS)
RE.CNT 24 THERE ARE 24 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 33 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1999:12961 CAPLUS <<LOGINID::20100917>>
DN 130:218913
TI Cloning of .alpha.-amylase gene from Schwanniomyces occidentalis and expression in Saccharomyces cerevisiae
AU Wang, Yongji; Liu, Hongdi; Sun, Tong; Zhang, Shuzheng
CS Institute Microbiology, Chinese Academy Sciences, Beijing, 100080, Peop. Rep. China
SO Science in China, Series C: Life Sciences (1998), 41(6), 569-575 CODEN: SCCLFO; ISSN: 1006-9305
PB Science in China Press
DT Journal
LA English
AB The cloning of .alpha.-amylase gene of S. occidentalis and the construction of starch digestible strain of ***yeast*** , S. ***cerevisiae*** AS. 2. 1364 with ethanol-tolerance and without ***auxotrophic*** markers used in fermn. industry were studied. The yeast/E. coli shuttle plasmid YCEp1 partial library of S. occidentalis DNA was constructed and .alpha.-amylase gene was screened in S. cerevisiae by amylolytic activity. Several transformants with amylolysis were obtained and one of the fusion plasmids had an about 5.0 kb inserted DNA fragment, contg. the upstream and downstream sequences of .alpha.-amylase gene from S. occidentalis. It was further confirmed by PCR and sequence detn. that this 5.0 kb DNA fragment contains the whole coding sequence of .alpha.-amylase. The amylolytic ***test*** showed that when this transformant was incubated on plate of YPDS medium contg. 1% glucose and 1% starch at 30.degree.C for 48 h starch degrdn. zones could be visualized by staining with iodine vapor. .alpha.-Amylase activity of the culture filtrate is 740-780 mU/mL and PAGE shows that the yeast harboring fusion plasmids efficiently secreted .alpha.-amylase into the medium, and the amt. of the recombinant .alpha.-amylase is more than 12% of the total proteins in the culture filtrate. These results showed that .alpha.-amylase gene can be highly expressed and efficiently secreted in S. cerevisiae AS. 2. 1364, and the promoter and the terminator of .alpha.-amylase gene from S. occidentalis work well in S. cerevisiae AS. 2. 1364.
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 34 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:796563 CAPLUS <<LOGINID::20100917>>
DN 130:149393
TI Growth inhibition of Saccharomyces cerevisiae by the immunosuppressant leflunomide is due to the inhibition of uracil uptake via Fur4p
AU Fujimura, H.
CS Laboratory of Advanced Technology, Discovery Research Laboratories, Nippon Hoechst Marion Roussel, Kawagoe, Japan

SO Molecular and General Genetics (1998), 260(1), 102-107 CODEN: MGGEAE; ISSN: 0026-8925
PB Springer-Verlag
DT Journal
LA English
AB The immunosuppressant leflunomide inhibits cytokine-stimulated proliferation of lymphoid cells in vitro and also inhibits the growth of the eukaryotic microorganism Saccharomyces cerevisiae. To elucidate the mol. mechanism of action of the drug, two yeast genes which suppress the anti-proliferative effect when ***present*** in multiple copies were cloned and designated MLF1 and MLF2 for multicopy suppressor of leflunomide sensitivity. DNA sequencing anal. revealed that the MLF1 gene is identical to the FUR4 gene, which encodes a uracil permease and functions to import uracil efficiently. The MLF2 was found to be identical to the URA3 gene. Excess exogenous uracil also overcomes the anti-proliferative effect of leflunomide on yeast cells. Uracil prototrophy also conferred resistance to leflunomide. Uracil uptake was inhibited by leflunomide. Thus, the growth inhibition by leflunomide seen in a S. ***cerevisiae*** ura3 ***auxotroph*** is due to the inhibition of the entry of exogenous uracil via the Fur4 uracil permease.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)
RE.CNT 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 35 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:722098 CAPLUS <<LOGINID::20100917>>
DN 130:78541
TI Threonine aldolase overexpression plus threonine supplementation enhanced riboflavin production in Ashbya gossypii
AU Monschau, Nicole; Sahm, Hermann; Stahmann, K.-Peter
CS Institut Biotechnologie 1, Forschungszentrum Julich GmbH, Julich, D-52425, Germany
SO Applied and Environmental Microbiology (1998), 64(11), 4283-4290 CODEN: AEMIDF; ISSN: 0099-2240
PB American Society for Microbiology
DT Journal
LA English
AB Riboflavin prodn. in the filamentous fungus Ashbya gossypii is limited by glycine, an early precursor required for purine synthesis. We report an improvement of riboflavin prodn. in this fungus by overexpression of the glycine biosynthetic enzyme threonine aldolase. The GLY1 gene encoding the threonine aldolase of A. gossypii was isolated by heterologous complementation of the glycine- ***auxotrophic*** ***Saccharomyces*** ***cerevisiae*** strain YM13 with a genomic library from A. gossypii. The deduced amino acid sequence of GLY1 showed 88% similarity to threonine aldolase from S. cerevisiae. In the ***presence*** of the GLY1 gene, 25 mU of threonine aldolase specific activity mg-1 was detectable in crude exts. of S. cerevisiae YM13. Disruption of GLY1 led to a complete loss of threonine aldolase activity in A. gossypii crude exts., but growth of and riboflavin prodn. by the knockout mutant were not affected. This indicated a minor role of the enzyme in glycine biosynthesis of A. gossypii. However, overexpression of GLY1 under the control of the constitutive TEF promoter and terminator led to a 10-fold increase of threonine aldolase specific activity in crude exts. along with a 9-fold increase of riboflavin prodn. when the medium was supplemented with threonine. This strong enhancement, which could not be achieved by supplementation with glycine alone, was attributed to an almost quant. uptake of threonine and its intracellular conversion into glycine. This became evident by a subsequent partial efflux of the glycine formed.
OSC.G 25 THERE ARE 25 CAPLUS RECORDS THAT CITE THIS RECORD (25 CITINGS)
RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 36 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:686869 CAPLUS <<LOGINID::20100917>>
DN 130:33651
TI Two novel gene expression systems based on the yeasts Schwanniomyces occidentalis and Pichia stipitis
AU Piontek, M.; Hagedorn, J.; Hollenberg, C. P.; Gellissen, G.; Strasser, A. W. M.
CS Rhein Biotech GmbH, Dusseldorf, 40595, Germany
SO Applied Microbiology and Biotechnology (1998), 50(3), 331-338 CODEN: AMBIDG; ISSN: 0175-7598
PB Springer-Verlag
DT Journal
LA English
AB Two non-Saccharomyces yeasts have been developed as hosts for heterologous gene expression. The celD gene from Clostridium thermocellum, encoding a heat-stable cellulase, served as the ***test*** sequence. The first system is based on the amylolytic species Schwanniomyces occidentalis, the second on the xylolytic species Pichia stipitis. The systems comprise auxotrophic host strains (trp5 in the case of S. occidentalis; trp5-10, his3 in the case of P. stipitis) and suitable transformation vectors. Vector components consist of an S. occidentalis-derived autonomously replicating sequence (SwARS) and the Saccharomyces cerevisiae-derived TRP5 sequence for plasmid propagation and selection in the yeast hosts, an ori and an ampicillin-resistance sequence for propagation and selection in a bacterial host. A range of vectors has been engineered employing different promoter elements for heterologous gene expression control in both species. Homologous elements derived from highly expressed genes of the resp. hosts appeared to be of superior quality: in the case of S. occidentalis that of the GAM1 gene, in the case of P. stipitis that of the XYL1 gene. Further elements ***tested*** are the S. cerevisiae-derived ADH1 and PDC1 promoter sequences.
OSC.G 28 THERE ARE 28 CAPLUS RECORDS THAT CITE THIS RECORD (28 CITINGS)
RE.CNT 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 37 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:639310 CAPLUS <<LOGINID::20100917>>
DN 130:49640
TI Incorporation of extracellular phospholipids and their effect on the growth and lipid metabolism of the Saccharomyces cerevisiae cho1/pss mutant
AU Yon, Jei-Oh; Nakamura, Hidemitsu; Ohta, Akinori; Takagi, Masamichi
CS Department of Biotechnology, The University of Tokyo, Bunkyo-ku, Tokyo, 113-8657, Japan
SO Biochimica et Biophysica Acta, Lipids and Lipid Metabolism (1998), 1394(1), 23-32 CODEN: BBLLA6; ISSN: 0005-2760
PB Elsevier B.V.
DT Journal

LA English
AB The cho1/pss mutant of ***Saccharomyces*** ***cerevisiae*** , which is ***auxotrophic*** for choline or ethanolamine because of the deficiency in phosphatidylserine synthesis, grew in the ***presence*** of 0.05 mM phosphatidylcholine (PC) contg. octanoic acids (diC8PC) or decanoic acids (diC10PC), but not in the ***presence*** of PC contg. longer acyl residues. It did not grow in the ***presence*** of the sol. hydrolytic products of PC, phosphorylcholine or glycerophosphorylcholine, at comparable concns. Addn. of 10 mM hemicholinium-3, a choline transport inhibitor, or disruption of the CTR gene, which encodes a choline transporter, inhibited the growth of the cho1/pss mutant in the ***presence*** of choline, but not in the ***presence*** of 0.1 mM diC8PC. Under diC8PC-supported growth conditions, octanoic acid was barely detectable in the cellular phospholipid fraction, but was recovered in the culture medium as the free acid, and the phosphatidylethanolamine (PE) content was low in comparison to choline-supported conditions. These results suggest that PCs with short acyl residues were taken up by the cho1/pss mutant and remodeled as they were used, and that PCs with short acyl residues do not inhibit conversion of PE to PC. The current results provide a new direction in the anal. of intracellular phospholipid movement and metab. in yeast.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 38 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:628131 CAPLUS <<LOGINID::20100917>>
DN 129:313214
OREF 129:63849a,63852a
TI Effect of squalene synthase gene disruption on synthesis of polyprenols in Saccharomyces cerevisiae
AU Grabowska, Dorota; Karst, Francis; Szkopinska, Anna
CS Institute of Biochemistry and Biophysics, PAN, Warsaw, 02-106, Pol.
SO FEBS Letters (1998), 434(3), 406-408 CODEN: FEBLAL; ISSN: 0014-5793
PB Elsevier Science B.V.
DT Journal
LA English
AB Biosynthesis of polyprenols was investigated in a wild-type strain of ***Saccharomyces*** ***cerevisiae*** and a squalene synthase-deficient strain ***auxotrophic*** for ergosterol. The quant. data showed that disruption of the squalene synthase gene caused a 6-fold increase in the synthesis of polyprenols in vitro in comparison with the wild-type strain. Microsomal prepn. from the deleted strain only slightly reacted to the addnl. exogenous FPP, while that from the wild-type strain ***presented*** a 4-fold increase of polyprenol synthesis. Restoration of ergosterol synthesis, by introducing ERG9 functional allele into the deleted strain, resulted in a significant lowering of polyprenol synthesis, indicating the immediate shift of the common substrate (FPP) to the sterol pathway. The role of squalene synthase in the regulation of polyprenol synthesis and 'flow diversion hypothesis' is discussed.
OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)
RE.CNT 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 39 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:559507 CAPLUS <<LOGINID::20100917>>
DN 129:255835
OREF 129:51995a,51998a
TI AILV1 gene from the yeast Arxula adeninivorans LS3-a new selective transformation marker
AU Wartmann, Thomas; Rosel, Harald; Kunze, Irene; Bode, Rudiger; Kunze, Gotthard
CS Institute Plant Genetics and Crop Plant Research, Gatersleben, D-06466, Germany
SO Yeast (1998), 14(11), 1017-1025 CODEN: YESTE3; ISSN: 0749-503X
PB John Wiley & Sons Ltd.
DT Journal
LA English
AB The ILV1 gene of the yeast Arxula adeninivorans LS3 (AILV1) has been cloned from a genomic library, characterized and used as an ***auxotrophic*** selection marker for transformation of plasmids into this ***yeast*** . One copy of the gene is ***present*** in the Arxula genome, comprising 1653 bp and encoding 550 amino acids of the threonine deaminase. The protein sequence is similar (60.55%) to that of the threonine deaminase from Saccharomyces cerevisiae encoded by the gene ILV1. The protein is enzymically active during the whole period of cultivation, up to 70 h. Maximal activities, as well as protein concns. of this enzyme, were achieved after cultivation times of 20-36 h. The AILV1 gene is a suitable auxotrophic selection marker in transformation expts. using an Arxula adeninivorans ilv1 mutant and a plasmid contg. this gene, which is fused into the 25S rDNA of Arxula adeninivorans. One to three copies of the linearized plasmid were integrated into the 25S rDNA by homologous recombination. Transformants resulting from complementation of the ilv1 mutation can be easily and reproducibly selected and in addn. are mitotically stable. Therefore, the described system is preferred to the conventional selection for hygromycin B resistance.
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)
RE.CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 40 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:537925 CAPLUS <<LOGINID::20100917>>
DN 129:172918
OREF 129:35081a,35084a
TI Biosynthesis of glycine as a precursor of riboflavin in Ashbya gossipii
AU Monschau, Nicole
CS Inst. Biotechnol., Forschungszentrum Juelich G.m.b.H., Juelich, D-52425, Germany
SO Berichte des Forschungszentrums Juelich (1998), Juel-3519, 1-115 pp. CODEN: FJBEE5; ISSN: 0366-0885
DT Report
LA German
AB The filamentous fungus Ashbya gossipii is a vitamin B2 overproducer. Enhancement of riboflavin prodn. is known to be achieved by supplementation of the medium with Gly, a precursor of vitamin B2 (riboflavin). The work describes the characterization and deregulation of Gly biosynthetic pathways in A. gossipii leading to an improved riboflavin prodn. In the A. gossipii wild type strain ATCC 10895 supplementation with 80 mM Gly lead to an increase in riboflavin prodn. by at least 100% whereas the growth remained unchanged. Nevertheless only 5%

of the added Gly were consumed during the course of cultivation, which suggested a poor uptake of the amino acid. On unsupplemented media Gly concn. even increased from 1.9 mM to 3 mM during cultivation. Consequently the effect of Gly on riboflavin prodn. can be attributed to a small net uptake as well as to an inhibition of Gly efflux due to the high extracellular Gly concn. The Gly biosynthetic enzymes Ser hydroxymethyltransferase, Thr aldolase, and Glu glyoxylate aminotransferase were detected in crude exts. of A. gossipii with max. specific activities of 6, 5, and 26 mU/mg protein, resp. Sucrose d. gradient centrifugation of A. gossipii organelles showed, that Glu glyoxylate aminotransferase occurs in the mitochondria of the fungus, thus it is not colocated with isocitrate lyase - the main supplier of glyoxylate - in the peroxisomes. Gly formation starting from Ser and Thr could also be demonstrated in vivo using 13C labeling expts. Likewise the formation of Ser from Thr, which probably proceeds via Gly and therefore means an unwanted loss of Gly, was shown in vivo. When 70 mM aminomethylphosphonic acid (AMPS) were added to the culture medium riboflavin prodn. of A. gossipii was completely inhibited. Screening on AMPS resistance of riboflavin prodn. lead to the isolation of the strain A.g. AMPS-NM-01. It showed a riboflavin prodn. of 40 mg/g mycelial dry wt. (mdw) even in the ***absence*** of Gly, which was significantly higher than in the wild type strain (5 mg/g mdw) under the same conditions but resembled wild type riboflavin prodn. in the ***presence*** of 80 mM of Gly (30 mg/g mdw). Increased riboflavin prodn. without Gly supplementation suggested a better intracellular availability of Gly in the mutant strain. Nevertheless, even in this case riboflavin prodn. could be increased by Gly supplementation to 95 mg/g mdw. In comparison to the wild type strain Ser hydroxy-methyltransferase specific activity was significantly reduced from 3 to 1.5 mU/mg protein in the strain A.g. AMPS-NM-01. Therefore the increased riboflavin prodn. of this strain can be explained by a better intracellular availability of Gly conditioned by a reduced loss of Gly for the formation of Ser. Using heterologous complementation of a ***Saccharomyces*** ***cerevisiae*** mutant ***auxotrophic*** for Gly a GLY1 homologous gene with unknown function was isolated from A. gossipii. Characterization of the corresponding enzymic activity showed that the isolated gene as well as the GLY1 gene from S. cerevisiae encode a Thr aldolase. In contrast to S. ***cerevisiae*** the GLY1 knock-out mutant of A. gossipii was not ***auxotrophic*** for Gly, which demonstrated that Thr aldolase plays only a minor role during Gly biosynthesis of A. gossipii. GLY1 was overexpressed in A. gossipii under the control of the TEF-promoter and -terminator using the expression vector pAG203. In crude exts. of A.g. pAG203GLY1 50 mU/mg protein of Thr aldolase specific activity were detected indicating atenfold overexpression in comparison to the wild type. When 50 mM Thr was fed to A.g. pAG203GLY1 an increase in riboflavin prodn. from 2 to 16 mg/g mdw was detd., an increase never reached with Gly because of its worse uptake. Thr was found to be taken up efficiently by this strain. Its conversion to Gly was confirmed by a striking efflux of Gly into the medium. Extracellular Gly correspondingly increased from 2 to 44 mM. The requirement to feed Thr in addn. to Thr aldolase overexpression demonstrated a limitation in Thr biosynthesis, which was confirmed by feeding expts. with Thr precursors.

L17 ANSWER 41 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:450394 CAPLUS <<LOGINID::20100917>>
DN 129:158965
OREF 129:32297a,32300a
TI Fatty acid desaturation in methylotrophic ***yeast*** Hansenula polymorpha strain CBS 1976 and unsaturated fatty acid ***auxotrophic*** mutants
AU Anamnart, Sarintip; Tolstorukov, Ilya; Kaneko, Yoshinobu; Harashima, Satoshi
CS Department of Biotechnology, Graduate School of Engineering, Osaka University, Suita, 565-0871, Japan
SO Journal of Fermentation and Bioengineering (1998), 85(5), 476-482 CODEN: JFBIEX; ISSN: 0922-338X
PB Society for Fermentation and Bioengineering, Japan
DT Journal
LA English
AB Anal. of fatty acid compn. in wild-type cells of Hansenula polymorpha strain CBS 1976 revealed the ***presence*** of 18:1(.DELTA.9), 18:2(.DELTA.9,12) and 18:3(.DELTA.9,12,15) unsatd. fatty acids (UFAs), indicating that the .alpha.-linolenic desatn. pathway operates in this yeast. H. polymorpha cells also showed ability for uptake and incorporation of exogenous UFAs. By Et methanesulfonate mutagenesis, nine unsatd. fatty acid auxotrophic mutants of H. polymorpha were isolated. These mutants exhibited the growth arrest phenotype on nutrient medium and on nutrient medium supplemented with satd. fatty acids, but grew on media supplemented with various UFAs. Genetic anal. revealed that single recessive nuclear mutation conferred Ufa auxotrophy on these mutants. Fatty acid anal. by gas chromatog. showed the accumulation of 18: 0 but a decrease in the amt. of 18: 1 and 18: 2 in mutant cells compared with the wild-type cells. Integrated physiol. and genetic data suggested that mutations in all mutants occurred in one gene and probably led to defects in .DELTA.9-desatn. pathway.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)
RE.CNT 37 THERE ARE 37 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 42 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:240313 CAPLUS <<LOGINID::20100917>>
DN 129:2571
OREF 129:627a,630a
TI Sterol uptake in ***Saccharomyces*** ***cerevisiae*** heme ***auxotrophic*** mutants is affected by ergosterol and oleate but not by palmitoleate or by sterol esterification
AU Ness, Frederique; Achstetter, Tilman; Duport, Catherine; Karst, Francis; Spagnoki, Roberto; Degryse, Eric
CS Yeast Department, Transgene S.A., Strasbourg, 67082, Fr.
SO Journal of Bacteriology (1998), 180(7), 1913-1919 CODEN: JOBAAY; ISSN: 0021-9193
PB American Society for Microbiology
DT Journal
LA English
AB The relationship between sterol uptake and heme competence in two yeast strains impaired in heme synthesis, namely, G204 and H12-6A, was analyzed. To evaluate heme availability, a heterologous 17.alpha.-hydroxylase cytochrome P 450 cDNA (P-450c17) was expressed in these strains, and its activity was measured in vivo. Heme deficiency in G204 led to accumulation of squalene and lethality. The heterologous cytochrome P 450 was inactive in this strain. The leaky H12-6A strain ***presented*** a slightly modified sterol content compared to that for the wild type, and the P-450c17 recovered partial activity. BY analyzing sterol transfer on nongrowing cells, it was shown that the cells were permeable toward exogenous cholesterol when they were depelted of endogenous sterols, which was the case for G204 but not for H12-6A. It was

concluded that the fully blocked heme mutant (G204) replenishes its diminishing endogenous sterol levels during growth by replacement with sterol from the outside medium. Endogenous sterol biosynthesis appears to be the primary factor capable of excluding exogenous sterol. Oleate but not palmitoleate was identified as a component that reduced but did not prevent sterol transfer. Sterol transfer was only slightly affected by a lack of esterification. It is described herein how avoidance of the potential cytotoxicity of the early intermediates of the mevalonate pathway could be achieved by a secondary heme mutation in erg auxotrophs.
OSC.G 25 THERE ARE 25 CAPLUS RECORDS THAT CITE THIS RECORD (25 CITINGS)
RE.CNT 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 43 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:209263 CAPLUS <<LOGINID::20100917>>
DN 128:292840
OREF 128:57963a,57966a
TI In vivo functional discrimination between plant thioredoxins by heterologous expression in the yeast Saccharomyces cerevisiae
AU Mouaheb, Nabil; Thomas, Dominique; Verdoucq, Lionel; Monfort, Patrick; Meyer, Yves
CS Lab. Physiologie Vegetale Moleculaire, Unite Mixte de Recherche Centre Natl. de la Recherche Scientifique 5545, Univ. Perpignan, Perpignan, 66025, Fr.
SO Proceedings of the National Academy of Sciences of the United States of America (1998), 95(6), 3312-3317 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Whereas vertebrates possess only two thioredoxin genes, higher plants ***present*** a much greater diversity of thioredoxins. For example, Arabidopsis thaliana has five cytoplasmic thioredoxins (type h) and at least as many chloroplastic thioredoxins. The abundance of plant thioredoxins leads to the question whether the various plant thioredoxins play a similar role or have specific functions. Because most of these proteins display very similar activities on artificial or biol. substrates in vitro, an in vivo approach to answer this question was developed. The disruption of both of the two ***Saccharomyces*** ***cerevisiae*** thioredoxin genes leads to pleiotropic effects including methionine ***auxotrophy*** , H2O2 hypersensitivity, altered cell cycle characteristics, and a limited ability to use methionine sulfoxide as source of methionine. Eight plant thioredoxins (six cytoplasmic and two chloroplastic) were expressed in yeast trx1, trx2 double mutant cells and were analyzed the different phenotypes. Arabidopsis type h thioredoxin 2 efficiently restored sulfate assimilation whereas Arabidopsis type h thioredoxin 3 conferred H2O2 tolerance. All thioredoxins ***tested*** could complement for redn. of methionine sulfoxide, whereas only type h thioredoxins were able to complement the cell cycle defect. Thus, specific interactions between plant thioredoxins and their targets occur in vivo.
OSC.G 84 THERE ARE 84 CAPLUS RECORDS THAT CITE THIS RECORD (84 CITINGS)
RE.CNT 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 44 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:158756 CAPLUS <<LOGINID::20100917>>
DN 128:290903
OREF 128:57503a,57506a
TI Characterization of Saccharomyces cerevisiae ARO8 and ARO9 genes encoding aromatic aminotransferases I and II reveals a new aminotransferase subfamily
AU Iraqui, I.; Vissers, S.; Cartiaux, M.; Urrestarazu, A.
CS Laboratoire Physiologie Cellulaire Genetique Levures, Universite Libre Bruxelles, Brussels, B-1050, Belg.
SO Molecular & General Genetics (1998), 257(2), 238-248 CODEN: MGGEAE; ISSN: 0026-8925
PB Springer-Verlag
DT Journal
LA English
AB The ARO8 and ARO9 genes of ***Saccharomyces*** ***cerevisiae*** were isolated by complementation of the phenylalanine-tyrosine ***auxotrophy*** of an aro8 and aro9 double-mutant strain that is defective in arom. aminotransferases I (aro8) and II (aro9). The genes were sequenced, and deletion mutants were constructed and analyzed. The expression of ARO8 and ARO9 was studied. The deduced amino acid sequences of Aro8p and Aro9p suggest that the former is a 500-residue, 56,168-Da polypeptide and the latter a 513-residue, 58,516-Da polypeptide. They correspond, resp., to Yg1202p and Yhr137p, two putative proteins of unknown function revealed by systematic sequencing of the yeast genome. We show that arom. aminotransferases I and II are homologous proteins, members of aminotransferase subgroup I, and, together with three other proteins, they constitute within the subgroup a new subfamily of enzymes specialized for arom. amino acid and .alpha.-aminoadipate transamination. ARO8 expression is subject to the general control of amino acid biosynthesis. ARO9 expression is induced when arom. amino acids are ***present*** in the growth medium and also in aro8 mutants grown on minimal ammonia medium. An autonomously replicating sequence (ARS) element is located between the ARO8 gene and YGL201c which encodes a protein of the minichromosome maintenance family.
OSC.G 30 THERE ARE 30 CAPLUS RECORDS THAT CITE THIS RECORD (30 CITINGS)
RE.CNT 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 45 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:114488 CAPLUS <<LOGINID::20100917>>
DN 128:215431
OREF 128:42621a
TI Pleiotropism of Tn5-induced mutants of Xanthomonas campestris pv. vesicatoria
AU Goncalves, Edmilson R.; Rosato, Yoko B.
CS Departamento de Genetica e Evolucao, Instituto de Biologia e CBMEG-UNICAMP, Campinas, 13083-970, Brazil
SO Summa Phytopathologica (1997), 23(3-4), 207-212 CODEN: SUPHDV; ISSN: 0100-5405
PB Grupo Paulista de Fitopatologia
DT Journal
LA English
AB Eleven Tn5-induced non-pathogenic mutants on tomato were isolated from Xanthomonas campestris pv. vesicatoria 479N. All the mutants were also ***tested*** for pathogenicity on pepper, hypersensitivity on tobacco, auxotrophy, growth curve and extracellular enzymes prodn. (amylase, cellulase, pectinase and protease). According to these

characteristics the mutants were classified in five groups. Group I, represented by the mutants 901, 905, 906 e 908, showed non-pathogenicity for both compatible hosts, tomato and pepper; group II (mutant 902) ***presented*** ***auxotrophy*** for a component of the ***yeast*** ext. and was white colored; group III (mutants 904, 910 and 911) ***presented*** no pectinase prodn.; group IV (mutants 907 and 909) remained pathogenic for pepper only and finally group V (mutant 903) was like group IV but lacking pectinase activity. Anal. of these mutants and complementation with a genomic library of the wild type strain will allow the detg. of the role of the auxotrophy and pectinase prodn. in the pathogenicity and cloning of determinants involved in the specific recognition of tomato as a host.
RE.CNT 25 THERE ARE 25 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 46 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1998:94203 CAPLUS <<LOGINID::20100917>>
DN 128:202803
OREF 128:40047a,40050a
TI TAT1 encodes a low-affinity histidine transporter in Saccharomyces cerevisiae
AU Bajmoczi, Milan; Sneve, Mary; Eide, David J.; Drewes, Lester R.
CS Department of Biochemistry & Molecular Biology, School of Medicine, University of Minnesota-Duluth, Duluth, MN, 55812, USA
SO Biochemical and Biophysical Research Communications (1998), 243(1), 205-209 CODEN: BBRCA9; ISSN: 0006-291X
PB Academic Press
DT Journal
LA English
AB Previous studies have revealed the ***presence*** of at least two histidine uptake systems in S. cerevisiae; one with high affinity and the other with low affinity for histidine. The HIP1 gene is known to encode the high affinity permease. The purpose of this study was to identify the gene that encodes the low affinity permease. A mutant strain of S. ***cerevisiae*** that is both a histidine ***auxotroph*** and a hip1 deletion mutant is unable to grow on low histidine media. This strain was transformed with a yeast cDNA library constructed in a yeast expression vector. Transformants with increased histidine transport were selected by their ability to grow on a low histidine media. Sequencing of the inserts revealed the ***presence*** of the HIP1 gene and also the ***presence*** of the TAT1 gene. Estd. KM and Vmax values for histidine transport by each system were detd. In a hip1 tat1 double mutant, the level of histidine required for growth increased eight-fold in comparison to the hip1 single mutant. Our results suggest that the TAT1-encoded protein, previously characterized as the high-affinity tyrosine permease, also acts as the low affinity histidine permease.
OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)
RE.CNT 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 47 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:672753 CAPLUS <<LOGINID::20100917>>
DN 127:343699
OREF 127:67387a,67390a
TI A ***yeast*** sterol ***auxotroph*** (erg25) is rescued by addition of azole antifungals and reduced levels of heme
AU Gachotte, D.; Pierson, C. A.; Lees, N. D.; Barbuch, R.; Koegel, C.; Bard, M.
CS Dep. Biol., Indiana Univ.-Purdue Univ., Indianapolis, IN, 46202, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1997), 94(21), 11173-11178 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB Genetic disruption of the Saccharomyces ***cerevisiae*** C-4 sterol Me oxidase ERG25 gene leads to sterol ***auxotrophy*** . The authors have characterized a suppression system that requires two mutations to restore viability to this disrupted strain. One suppressor mutation is erg11, which is blocked in 14.alpha.-demethylation of lanosterol and is itself an auxotrophy. The second suppressor mutation required is either slu1 or slu2 (suppressor of lanosterol utilization). These mutations are leaky versions of HEM2 and HEM4, resp.; addn. of exogenous hemin reverses the suppressing effects of slu1 and slu2. Suppression of erg25 by erg11 slu1 (or erg11 slu2) results in a slow-growing strain in which lanosterol, the first sterol in the pathway, accumulates. This result indicates that endogenously synthesized lanosterol can substitute for ergosterol and support growth. In the triple mutants, all but 1 (ERG6) of the 13 subsequent reactions of the ergosterol pathway are inactive. Azole antibiotics (clotrimazole, ketoconazole, and itraconazole) widely used to combat fungal infections are known to do so by inhibiting the ERG11 gene product, the 14.alpha.-demethylase. Thus, treatment of the sterol auxotrophs erg25 slu1 or erg25 slu2 with azole antibiotics paradoxically restores viability to these strains in the ***absence*** of sterol supplementation via the suppression system described here.
OSC.G 21 THERE ARE 21 CAPLUS RECORDS THAT CITE THIS RECORD (21 CITINGS)
RE.CNT 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 48 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:663724 CAPLUS <<LOGINID::20100917>>
DN 127:355873
OREF 127:69603a,69606a
TI Suppression of the Saccharomyces cerevisiae hac1/ire15 mutation by yeast genes and human cDNAs
AU Nikawa, Jun-ichi; Sugiyama, Minetaka; Hayashi, Kunihiro; Nakashima, Asae
CS Department of Biochemical Engineering and Science, Faculty of Computer Science and Systems Engineering, Kyushu Institute of Technology, Iizuka, Japan
SO Gene (1997), 201(1-2), 5-10 CODEN: GENED6; ISSN: 0378-1119
PB Elsevier
DT Journal
LA English
AB We previously reported that the ***Saccharomyces*** ***cerevisiae*** ire15 mutation results in an inositol-***auxotrophic*** phenotype, and that human cDNAs can suppress the ire15 mutation. Herein, we ***present*** evidence that the gene responsible for the ire15 mutation is HAC1, which encodes a transcription factor for KAR2, obtained by isolating a yeast single-copy suppressor gene and by performing

complementation anal. Sequencing anal. revealed that the mutant HAC1 gene obtained from the ire15 mutant contained an AAA codon at position 50 instead of the AGA codon obsd. in the wild-type gene, resulting in the alteration of the aa from Arg to Lys. All human cDNAs and yeast multicopy suppressors, which had been isolated as suppressors for the ire15 mutation, were able to suppress the inositol-auxotrophic phenotype but not the defect in KAR2 induction of the hac1-disrupted strain.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)
RE.CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 49 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:518925 CAPLUS <<LOGINID::20100917>>
DN 127:233571
OREF 127:45579a,45582a
TI Biosynthesis of .alpha.-ketoglutaric acid from ethanol by yeasts
AU Chernyavskaya, O. G.; Shishkanova, N. V.; Finogenova, T. V.
CS Russian Acad. Sci., Inst. Microbiol. Biochem. Microorganisms, Moscow, 142292, Russia
SO Prikladnaya Biokhimiya i Mikrobiologiya (1997), 33(3), 296-300 CODEN: PBMIAK; ISSN: 0555-1099
PB MAIK Nauka
DT Journal
LA Russian
AB Twenty yeast strains were ***tested*** for their ability to synthesize .alpha.-ketoglutaric acid from ethanol. Only thiamine- ***auxotrophic*** ***yeast*** strains belonging to different genera (Candida, Yarrowia, and Pichia) and species were shown to produce .alpha.-ketoglutaric acid. Limitation of yeast growth by reduced thiamine was necessary for the synthesis of .alpha.-ketoglutaric acid. Yarrowia lipolytica N1, which accumulated 40-48 g/l of .alpha.-ketoglutaric acid with a yield of 40-44% of ethanol consumed, was selected as the most active producer of .alpha.-ketoglutaric acid. Optimum conditions for the synthesis of .alpha.-ketoglutaric acid from ethanol (thiamine concn., pH of the culture medium, and the dissolved oxygen concn. in the medium) were studied.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L17 ANSWER 50 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:517821 CAPLUS <<LOGINID::20100917>>
DN 127:133220
OREF 127:25637a,25640a
TI Conditions that induce revertants at high frequency at leu locus of an ***auxotrophic*** diploid mutant of ***yeast***
AU Uchida, Akira
CS Fac. Hum. Dev., Kobe Univ., Kobe, 657, Japan
SO Kobe Daigaku Hattatsu Kagakubu Kenkyu Kiyo (1997), 4(2), 425-429 CODEN: KDHKEW; ISSN: 0919-7419
PB Kobe Daigaku Hattatsu Kagakubu
DT Journal
LA English
AB In relation to adaptive mutation, patterns were examd. of reverse mutations in a nutrition-requiring mutant of Saccharomyces cerevisiae that required adenine, uracil, leucine and lysine. The reversion of the leu- gene to leu+ occurred with high frequency when cells were shifted down from complete to minimal liq. medium. By using starvation for amino acids and nitrogenous bases in liq. media, different reversion patterns were obsd. Although the frequencies varied with the combinations of withheld nutrients, high reversion rates of the leu- locus were also obsd. However, they were repressed when leucine was ***present*** in the starvation medium. The reversion rates of ura and lys genes were not affected by the shiftdown in the culture medium and by the starvation for nutrients.

L17 ANSWER 51 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:488123 CAPLUS <<LOGINID::20100917>>
DN 127:118262
OREF 127:22713a,22716a
TI Auxotrophic mutant starter and feeder cells in cross-feeding system with reversibly noninfective modified lambdoid bacteriophage to produce colony containing starter cells that excrete a desired protein
IN Ray, Bryan L.; Lin, Edmund C. C.; Crea, Roberto
PA President and Fellows of Harvard College, USA
SO U.S., 34 pp., Cont.-in-part of U.S. 5,348,872. CODEN: USXXAM
DT Patent
LA English
FAN.CNT 3 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI US 5646030 A 19970708 US 1994-294386 19940823 US 5348872 A 19940920 US 1992-991115 19921216 WO 9606164 A1 19960229 WO 1995-US10224 19950810 W: AU, CA, JP RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE AU 9533635 A 19960314 AU 1995-33635 19950810
PRAI US 1990-541895 B1 19900621 US 1992-856876 B2 19920324 US 1992-991115 A2 19921216 US 1994-294386 A 19940823 WO 1995-US10224 W 19950810
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB Disclosed is a method for isolating a mutant cell that excretes a desired compd. The method includes culturing a plurality of auxotrophic pretreated starter cells and auxotrophic feeder cells in the ***presence*** of a reversibly noninfective, modified lambdoid bacteriophage. If the treated starter cell produces the desired compd., the bacteriophage will be rendered infective and infect the feeder cell. The feeder cell, in turn, will excrete a metabolite required by the starter cell and the starter cell will excrete a metabolite required by the feeder cell, enabling the cells to cross-feed, grow, and produce a colony contg. a starter cell which produces the desired compd. The method takes advantage that lambdoid bacteriophage having a target mol. peptide linked to the glycoprotein gpV gene can be successfully assembled in vivo such that the target mol. is displayed on the outer surface of the bacteriophage. The method is illustrated by using the chem. modified bacteriophage .lambda. for (1) screening treated bacteria for prodn. of ciliary neurotrophic factor or interleukin-1.beta. converting enzyme, (2) screening genetically engineered yeast producing erythropoietin, (3) screening Corynebacterium glutamicum for prodn. of staphylococcal nuclease, (4) isolation of a transformed human Bj-cell producing antibodies to hepatitis C virus, and (5) isolation of digitalis lanata plant cells producing quinine.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 52 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:425264 CAPLUS <<LOGINID::20100917>>
DN 127:30136
OREF 127:5709a,5712a
TI ***Yeast*** chitin synthase 1 gene sequence, recombinant vector and ***auxotrophic*** host cell, and method for determining growth-associated proteins and genetic elements
IN Koltin, Yigal; Riggle, Perry; Gavrias, Vicky; Bulawa, Chris; Winter, Ken
PA Chemgenics Pharmaceuticals, Inc., USA
SO PCT Int. Appl., 64 pp. CODEN: PIXXD2
DT Patent
LA English
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 9716540 A1 19970509 WO 1996-US17459 19961101 W: CA, JP RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE US 5824545 A 19981020 US 1995-551437 19951101 CA 2233881 A1 19970509 CA 1996-2233881 19961101 EP 862618 A1 19980909 EP 1996-938696 19961101 R: BE, CH, DE, DK, ES, FR, GB, IT, LI, SE, FI JP 11514885 T 19991221 JP 1996-517538 19961101 US 6020133 A 20000201 US 1998-4225 19980108 US 6251593 B1 20010626 US 1998-84346 19980527 US 6291218 B1 20010918 US 1998-104704 19980625
PRAI US 1995-551437 A 19951101 WO 1996-US17459 W 19961101 US 1998-4225 A3 19980108
ASSIGNMENT HISTORY FOR US PATENT AVAILABLE IN LSUS DISPLAY FORMAT
AB A polynucleotide encoding chitin synthase (CHS1), an enzyme essential for cell wall synthesis and yeast cell growth, is provided. A maltose responsive promoter (MRP) isolated using the promoter library of the invention is also described. The ***present*** invention also provides a vector for isolation of a eukaryotic regulatory polynucleotide, i.e., promoter. The vector is useful in the method of the invention which comprises identifying a eukaryotic regulatory polynucleotide, i.e., promoter region, by complementing the growth of an auxotrophic host cell contg. the vector of the invention, which includes a promoter region operably linked to a promoterless auxotrophic gene.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L17 ANSWER 53 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1997:397743 CAPLUS <<LOGINID::20100917>>
DN 127:91319
OREF 127:17461a,17464a
TI Starvation for a specific amino acid induces high frequencies of rho- mutants in Saccharomyces cerevisiae
AU Heidenreich, Erich; Wintersberger, Ulrike
CS Dep. of Mol. Genet., Inst. of Tumor Biol. and Cancer Res., Univ. of Vienna, Vienna, A-1090, Austria
SO Current Genetics (1997), 31(5), 408-413 CODEN: CUGED5; ISSN: 0172-8083
PB Springer
DT Journal
LA English
AB ***Auxotrophic*** ***yeast*** cells were starved on solid media for their resp. essential amino acid in the course of "adaptive mutation" expts. Thereby, high proportions of mitochondrial respiratory deficient (rho-) mutants accumulated among the cells stressed on selective plates. Using a strain with a plus-four frameshift mutation in a chromosomal gene involved in lysine biosynthesis, we obsd. that many of the revertant colonies which arose late under the selective pressure were composed of mixts. of rho+ and rho- cells, indicating that they originated from founder cells contg. intact as well as defective mitochondrial genomes. We show that in spite of the slower growth of rho- cells the late-appearing colonies cannot be interpreted as descending from rho- revertants ***present*** before selective plating.
OSC.G 17 THERE ARE 17 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)

L17 ANSWER 54 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:730852 CAPLUS <<LOGINID::20100917>>
DN 126:27508
OREF 126:5529a,5532a
TI Cloning of the ASN1 and ASN2 genes encoding asparagine synthetases in Saccharomyces cerevisiae: differential regulation by the CCAAT-box-binding factor
AU Dang, Van-Dinh; Valens, Michele; Bolotin-Fukuhara, Monique; Daignan-Fornier, Bertrand
CS Inst. de Genetique et Microbiologie, Univ. de Paris-Sud, Orsay, 91405, Fr.
SO Molecular Microbiology (1996), 22(4), 681-692 CODEN: MOMIEE; ISSN: 0950-382X
PB Blackwell
DT Journal
LA English
AB Two new yeast genes, named ASN1 and ASN2, were isolated by complementation of the growth defect of an asparagine auxotrophic mutant. Genetical anal. indicates that these two genes are allelic to the asnA and asnB loci described previously. Simultaneous disruption of both genes leads to a total asparagine auxotrophy, while disruption of asn1 or asn2 alone has no effect on growth under ***tested*** conditions. Nucleotide sequences of ASN1 and ASN2 revealed striking similarities with genes encoding asparagine synthetase (AS) from other organisms. Regulation of ASN1 and ASN2 expression was studied using lacZ fusions and both genes were found to be several times less expressed in the ***absence*** of the transcription activator Gcn4p. The HAP complex, another transcription factor that binds to CCAAT-box sequences, was shown to specifically affect ASN1 expression. Hap2p and Hap3p subunits of the HAP complex are required for optimal expression of ASN1, while the Hap4p regulatory subunit, which is required for regulation by the carbon source, plays a minor role in the process. Consistent with the weak effect of Hap4p, the carbon source does not significantly affect expression of ASN1. Our results show that the role of the HAP complex is not limited to activation of genes required for respiratory metab.
OSC.G 24 THERE ARE 24 CAPLUS RECORDS THAT CITE THIS RECORD (24 CITINGS)

L17 ANSWER 55 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:633768 CAPLUS <<LOGINID::20100917>>
DN 125:296053
OREF 125:55263a,55266a

TI Isolation by genetic complementation of two differentially expressed genes for .beta.-isopropylmalate dehydrogenase from Aspergillus niger
AU Williams, B. A.; Sillaots, S.; Tsang, A.; Storms, R.
CS Dep. of Biology, Concordia University, Montreal, QC, H3G 1M8, Can.
SO Current Genetics (1996), 30(4), 305-311 CODEN: CUGED5; ISSN: 0172-8083
PB Springer
DT Journal
LA English
AB We have constructed an Aspergillus niger cDNA library with a yeast expression vector. The library DNA complemented a leucine ***auxotroph*** of ***Saccharomyces*** ***cerevisiae*** (strain BWG1-7a) at a frequency of 4 .times. 10-4. Plasmids rescued from the yeast prototrophs also complemented Escherichia coli (strain MC1066) deficient in leucine biosynthesis. Sequence detn. of the rescued plasmids revealed two genes for .beta.-isopropylmalate dehydrogenase, which we called leu2A and leu2B. Genomic-blot anal. suggested that both leu2A and leu2B were derived from single-copy genes. Northern-blot hybridization showed that in nutrient-rich medium a leu2A transcript accumulated during germination and log-phase growth while the leu2B transcript appeared late in the growth phase. In minimal medium, only leu2A expression was greatly stimulated. We examd. the codon preference of these two genes. Whereas leu2A shows a bias in codon usage typical of A. niger genes, leu2B does not. These results indicate the ***presence*** in A. niger of two highly divergent, differentially regulated, isoenzymes for .beta.-isopropyl-malate dehydrogenase.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

L17 ANSWER 56 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:559400 CAPLUS <<LOGINID::20100917>>
DN 125:215153
OREF 125:40075a,40078a
TI Thi1, a thiamine biosynthetic gene in Arabidopsis thaliana, complements bacterial defects in DNA repair
AU Machado, C. R.; Costa de Oliveira, R. L.; Boiteux, S.; Praekelt, U. M.; Meacock, P. A.; Menck, C. F. M.
CS Depto. de Biologia, Instituto de Biociencias, Universidade de Sao Paulo, Sao Paulo, 05422-970, Brazil
SO Plant Molecular Biology (1996), 31(3), 585-593 CODEN: PMBIDB; ISSN: 0167-4412
PB Kluwer
DT Journal
LA English
AB An Arabidopsis thaliana cDNA was isolated by complementation of the Escherichia coli mutant strain BW535 (xth, nfo, nth), which is defective in DNA base excision repair pathways. This cDNA partially complements the Me methane sulfonte (MMS) sensitive phenotype of BW535. It also partially corrects the UV-sensitive phenotype of E. coli AB1886 (uvrA) and restores its ability to reactivate UV-irradiated .lambda. phage. It has an insert of ca. 1.3 kb with an open rading frame of 1047 bp (predicting a protein with a mol. mass of 36 kDa). This cDNA ***presents*** a high homol. to a stress related gene from two species of Fusarium (sti35) and to genes whose products participate in the thiamine biosynthesis pathway, THI4, from Saccharomyces cerevisiae and nmt2 from Schizosaccharomyces pombe. The Arabidopsis predicted polypeptide has homol. to several protein motifs: amino-terminal chloroplast transit peptide, dinucleotide binding site, DNA binding and bacterial DNA polymerases. The ***auxotrophy*** for thiamine in the ***yeast*** thi4::URA3 disruption strain is complemented by the Arabidopsis gene. Thus, the cloned gene, named thi1, is likely to function in the biosynthesis of thiamine in plants. The data ***presented*** in this work indicate that thi1 may also be involved in DNA damage tolerance in plant cells.
OSC.G 36 THERE ARE 36 CAPLUS RECORDS THAT CITE THIS RECORD (37 CITINGS)

L17 ANSWER 57 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:533966 CAPLUS <<LOGINID::20100917>>
DN 125:186861
OREF 125:34783a,34786a
TI A useful colony color phenotype associated with the yeast selected/counter-selectable marker MET15
AU Cost, Gregory J.; Boeke, Jef D.
CS Dep. of Molecular Biology and Genetics, Johns Hopkins Univ. Sch. of Med., Baltimore, MD, 21205, USA
SO Yeast (1996), 12(10), 939-941 CODEN: YESTE3; ISSN: 0749-503X
PB Wiley
DT Journal
LA English
AB Strain of ***Saccharomyces*** ***cerevisiae*** bearing null alleles of the Met15 gene are methionine ***auxotroph*** and become darkly pigmented in the ***presence*** of Pb2+ ions (Ono et al. (1991). Appl. Env. Microbiol. 57, 3183-3186). We describe the cloning of a useful fragment of the MET15 locus which complements both the methionine requirement and the colony color phenotype. This colony color phenotype is very useful for genetic screens and may be applicable for use in other yeast species. The combination of the size of MET15, along with its counter-selectability and the color of Met15 mutations make this perhaps the most versatile yeast genetic marker.
OSC.G 37 THERE ARE 37 CAPLUS RECORDS THAT CITE THIS RECORD (37 CITINGS)

L17 ANSWER 58 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:389247 CAPLUS <<LOGINID::20100917>>
DN 125:78270
OREF 125:14711a
TI The yeast BSD2-1 mutation influences both the requirement for phosphatidylinositol-transfer protein function and derepression of phospholipid biosynthetic gene expression in yeast
AU Kagiwada, Satoshi; Kearns, Brian G.; McGee, Todd P.; Fang, Min; Hosaka, Kohei; Bankaitis, Vytas A.
CS Department of Cell Biology, University of Alabama, Birmingham, AL, 35294-0005, USA
SO Genetics (1996), 143(2), 685-697 CODEN: GENTAE; ISSN: 0016-6731
PB Genetics Society of America
DT Journal
LA English
AB The BSD2-1 allele renders Saccharomyces cerevisiae independent of its normally essential requirement for phosphatidylinositol transfer protein (Sec14p) in the stimulation of Golgi secretory function and cell viability. We now report that BSD2-1 ***yeast*** mutants also exhibit yet another phenotype, an inositol ***auxotrophy*** . We demonstrate that the basis for this Ino- phenotype is the inability of BSD2-1 strains to derepress transcription of INO1, the structural gene for the enzyme that catalyzes the committed step in de novo inositol

biosynthesis in yeast. This constitutive repression of INO1 expression is mediated through specific inactivation of Ino2p, a factor required for trans-activation of INO1 transcription, and we show that these transcriptional regulatory defects can be uncoupled from the "bypass Sec14p" phenotype of BSD2-1 strains. Finally, we ***present*** evidence that newly synthesized phosphatidylinositol is subject to accelerated turnover in BSD2-1 mutants and that prevention of this accelerated phosphatidylinositol turnover in turn negates suppression of Sec14p defects by BSD2-1. We propose that, in BSD2-1 strains, a product(s) generated by phosphatidylinositol turnover coordinately modulates the activities of both the Sec14p/Golgi pathway and the pathway through which transcription of phospholipid biosynthetic genes is derepressed.
OSC.G 17 THERE ARE 17 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)

L17 ANSWER 59 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1996:274235 CAPLUS <<LOGINID::20100917>>
DN 124:308640
OREF 124:56999a,57002a
TI pH sensitivity of Schizosaccharomyces pombe: effect on the cellular phenotype associated with lacZ gene expression
AU Arndt, Greg M.; Atkins, David
CS R.W. Johnson Pharm. Res. Inst., Sydney, 2001, Australia
SO Current Genetics (1996), 29(5), 457-461 CODEN: CUGED5; ISSN: 0172-8083
PB Springer
DT Journal
LA English
AB We report on a series of expts. in Schizosaccharomyces pombe to detect the blue-color colony phenotype assocd. with expression of the Escherichia coli lacZ gene. Increasing the pH in solid minimal medium to optimize blue colony color revealed a pH-sensitive phenotype in auxotrophic strains requiring uracil and leucine as external supplements. This phenotype was obsd. among common S. pombe stock strains, 5-fluoroorotic acid (5-FOA)-selected strains, and random genetic segregants. Growth of prototrophic S. pombe strains 972 and 975 or the adenine auxotrophic strain NCYC 1860 were unaffected by an increase in external pH. Anal. of genetic segregants from three independent crosses indicated that a single ***auxotrophic*** marker (ura4- or leu1-32) was sufficient for ***yeast*** cell-growth inhibition when the medium pH was increased above 6.6. In contrast, growth of a Saccharomyces cerevisiae strain isogenic to AH22, requiring uracil, leucine and histidine, was unaffected by changes in the pH of the medium. These observations suggest that uptake of uracil and leucine into S. pombe cells is compromised by alterations in external pH. Our results have implications for detection of the lacZ gene-encoded blue color colony phenotype in S. pombe, which is optimized by growth in the ***presence*** of 5-bromo-4-chloro-3-indolyl-.beta.-D-galactoside (Xgal) at pH 7.0. We discuss the conditions under which this blue-color phenotype can be routinely obsd. in S. pombe.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L17 ANSWER 60 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1995:969965 CAPLUS <<LOGINID::20100917>>
DN 124:107946
OREF 124:19951a,19954a
TI Cloning plant genes by complementation of yeast mutants
AU d'Enfert, Christophe; Minet, Michele; Lacroute, Francois
CS Unite de Mycologie, Institut Pasteur, Paris, 75724, Fr.
SO Methods in Cell Biology (1995), 49, 417-30 CODEN: MCBLAG; ISSN: 0091-679X
DT Journal
LA English
AB The authors ***present*** the procedure used by Minet et.al.(1992) to construct an Arabidopsis thaliana cDNA expression library and transformation strategies that can be used to introduce the cDNA library into mutant Saccharomyces cerevisiae strains and to recover complementing plasmids. The method is highly efficient for identifying plant genes with functional yeast homologs and is not dependent upon any sequence homol. of the encoded proteins.
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L17 ANSWER 61 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1995:841665 CAPLUS <<LOGINID::20100917>>
DN 124:2120
OREF 124:479a,482a
TI Molecular cloning, characterization, and functional expression of rat oxidosqualene cyclase cDNA
AU Abe, Ikuro; Prestwich, Glenn D.
CS Dep. Chem., State Univ. New York, Stony Brook, NY, 11794-3400, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1995), 92(20), 9274-8 CODEN: PNASA6; ISSN: 0027-8424
PB National Academy of Sciences
DT Journal
LA English
AB A cDNA encoding rat oxidosqualene lanosterol-cyclase [lanosterol synthase; (S)-2,3-epoxysqualene mutase (cyclizing, lanosterol-forming), EC 5.4.99.7] was cloned and sequenced by a combination of PCR amplification, using primers based on internal amino acid sequence of the purified enzyme, and cDNA library screening by oligonucleotide hybridization. An open reading frame of 2199 bp encodes a Mr 83,321 protein with 733 amino acids. The deduced amino acid sequence of the rat enzyme showed significant homol. to the known oxidosqualene cyclases (OSCs) from yeast and plant (39-44% identity) and still retained 17-26% identity to two bacterial squalene cyclases (EC 5.4.99.-). Like other cyclases, the rat enzyme is rich in arom. amino acids and contains five so-called QW motifs, highly conserved regions with a repetitive .beta.-strand turn motif. The binding site sequence for the 29-methylidene-2,3-oxidosqualene (29-MOS), a mechanism-based irreversible inhibitor specific for the vertebrate cyclase, is well-conserved in all known OSC. The hydropathy plot revealed a rather hydrophilic N-terminal region and the ***absence*** of a hydrophobic signal peptide. Unexpectedly, this microsomal membrane-assocd. enzyme showed no clearly delineated transmembrane domain. A full-length cDNA was constructed and subcloned into a pYEUra3 plasmid, selected in Escherichia coli cells, and used to transform the OSC-deficient uracil- ***auxotrophic*** SGL9 strain of ***Saccharomyces*** ***cerevisiae*** . The recombinant rat OSC expressed was efficiently labeled by the mechanism-based inhibitor [3H]29-MOS.
OSC.G 63 THERE ARE 63 CAPLUS RECORDS THAT CITE THIS RECORD (63 CITINGS)

L17 ANSWER 62 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1995:311068 CAPLUS <<LOGINID::20100917>>
DN 122:257534

OREF 122:46805a,46808a
TI Cloning and sequence of the SCS3 gene which is required for inositol prototrophy in Saccharomyces cerevisiae
AU Hosaka, Kohei; Nikawa, Jun-ichi; Kodaki, Tsutomu; Ishizu, Hideki; Yamashita, Satoshi
CS Department Biochemistry, Gunma University School Medicine, Gunma, 371, Japan
SO Journal of Biochemistry (1994), 116(6), 1317-21 CODEN: JOBIAO; ISSN: 0021-924X
PB Japanese Biochemical Society
DT Journal
LA English
AB The SCS3 gene of Saccharomyces cerevisiae was cloned by functional complementation, using a conditional mutant exhibiting myo-inositol auxotrophy in the ***presence*** of choline, and sequenced. The sequence contained an open reading frame capable of encoding 380 amino acids with a calcd. mol. wt. of 42,734. Disruption of the SCS3 locus caused myo-inositol auxotrophy. The gene appeared to be involved in the synthesis of inositol phospholipids from inositol but not in the control of inositol synthesis.
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L17 ANSWER 63 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1995:284314 CAPLUS <<LOGINID::20100917>>
DN 122:125166
OREF 122:23211a,23214a
TI Occurrence of chromosome rearrangements during the fusion process in the imperfect yeast Candida albicans
AU Suzuki, Takahito; Yamada, Miho; Sakaguchi, Shuichi
CS Dep. Biol., Nara Women's Univ., Narashi, 630, Japan
SO Microbiology (Reading, United Kingdom) (1994), 140(12), 3319-28 CODEN: MROBEO; ISSN: 1350-0872
PB Society for General Microbiology
DT Journal
LA English
AB ***Auxotrophic*** derivs. of three strains of the pathogenic ***yeast*** Candida albicans of different origins, including 1006 derived from CBS5736, A5153 derived from FC18 and NARA2 derived from NUM961, were used in spheroplast fusion expts. The DNA content of the prototrophic fusion product obtained following fusion between strains 1006 and A5153 approximated to the sum of those of the parents, but was variable when NARA2 was used as the parent for fusion. Chromosome-sized DNA mols. of the fusion derivs. were sepd. by pulsed-field gel electrophoresis to examine whether either or both of the chromosome-sized DNA mols. of each parent were transfered into the fusion derivs. In the fusion derivs. obtained following fusion between strains 1006 and A5153, nearly the full complement of chromosomes was shown to be transferred, but partial transfer of chromosomes occurred in the fusion derivs. that were obtained following fusion between strains NARA2 and A5153. Results indicated that chromosome loss also occurred when these two strains were fused. Variations in the size of R chromosomes, the rDNA-contg. chromosomes, were obsd. in all fusion derivs. ***tested*** , indicating high-frequency recombination between R chromosomes during the fusion process.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L17 ANSWER 64 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1995:141073 CAPLUS <<LOGINID::20100917>>
DN 122:152884
OREF 122:28101a,28104a
TI Characterization of the Candida albicans TRP1 gene and construction of a homozygous trp1 mutant by sequential co-transformation
AU Ostrander, Darin B.; Gorman, Jessica A.
CS Department of Microbial Molecular Biology, Bristol-Myers Squibb Pharmaceutical Research Institute, Princeton, NJ, 08543-4000, USA
SO Gene (1994), 148(2), 179-85 CODEN: GENED6; ISSN: 0378-1119
PB Elsevier
DT Journal
LA English
AB The Candida albicans TRP1 gene has been isolated by complementation of an Escherichia coli trpC mutant. Sequence anal. has revealed a single ORF (open reading frame) of 678 nucleotides (nt). The amino acid (aa) sequence deduced from this coding region demonstrates a high degree of homol. with PRAI (phosphoribosylanthranilate isomerase) enzymes of other fungi, as well as bacterial species. The gene is also analogous to other yeast TRP1 genes in that it encodes a unifunctional enzyme, whereas TRP1 in filamentous fungi encodes a tri-functional enzyme. Both chromosomal copies of the gene were disrupted by sequential integrative transformation employing co-transformation of an ade1 mutant in order to create a homozygous auxotrophic trp1,ade1 C. albicans strain. This double ***auxotroph*** was used to ***test*** the ability of the ***Saccharomyces*** ***cerevisiae*** TRP1 gene to complement the C. albicans trp1 mutation; no expression of the S. cerevisiae gene was detectable.
OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)

L17 ANSWER 65 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1995:124450 CAPLUS <<LOGINID::20100917>>
DN 122:25193
OREF 122:4872h,4873a
TI Centromere promoter factors (CPF1) of the yeasts Saccharomyces cerevisiae and Kluyveromyces lactis are functionally exchangeable, despite low overall homology
AU Mulder, Wietse; Winkler, Aaron A.; Scholten, Inge H. J. M.; Zonneveld, Ben J. M.; de Winde, Johannes H.; de Steensma, H. Y.; Grivell, Leslie A.
CS Sect. Mol. Biol., Inst. Mol. Cell Biol., Amsterdam, NL-1098 SM, Neth.
SO Current Genetics (1994), 26(3), 198-207 CODEN: CUGED5; ISSN: 0172-8083
DT Journal
LA English
AB The KlCPF1 gene, coding for the centromere and promoter factor CPF1 from Kluyveromyces lactis, has been cloned by functional complementation of the methionine ***auxotrophic*** phenotype of a ***Saccharomyces*** ***cerevisiae*** mutant lacking ScCPF1. The amino-acid sequences of both CPF1 proteins show a relatively-low overall identity (31%), but a highly-homologous C-terminal domain (86%). This region constitutes the DNA-binding domain with basic-helix-loop-helix and leucine-zipper motifs, features common to the myc-related transcription factor family. The N-terminal two-thirds of the CPF1 proteins show no significant similarity, although the ***presence*** of acidic regions is a shared feature. In KlCPF1, the acidic region is a prominent stretch of approx. 40 consecutive aspartate and glutamate residues, suggesting that this part might be involved in transcriptional

activation. In-vitro mobility-shift expts. were used to establish that both CPF1 proteins bind to the consensus binding site RTCACRTG (CDEI element). In contrast to S. cerevisiae, CPF1 gene-disruption is lethal in K. lactis. The homologous CPF1 genes were transformed to both S. cerevisiae and K. lactis cpf1-null strains. Indistinguishable phenotypes were obsd., indicating that, not withstanding the long nonconserved N-terminal region, the proteins are sufficiently homologous to overcome the phenotypes assocd. with cpf1 gene-disruption.
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (16 CITINGS)

L17 ANSWER 66 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1995:11248 CAPLUS <<LOGINID::20100917>>
DN 122:27518
OREF 122:5361a
TI Formation of stable Ustilago hordei diploids
AU Harrison, Rhonda L.; Sherwood, John E.
CS Dep. Plant Pathol., Mont. State Univ., Bozeman, MT, 59717-0314, USA
SO International Journal of Plant Sciences (1994), 155(1), 15-22
CODEN: IPLSE2; ISSN: 1058-5893
DT Journal
LA English
AB During asexual growth, the fungus U. hordei reproduces as haploid uninucleate budding yeastlike cells (sporidia) that are nonpathogenic. Mating of sporidia, which is controlled by a single mating-type locus with 2 alleles, results in the formation of pathogenic dikaryotic mycelia. When sporidia of the opposite mating type with nonallelic ***auxotrophic*** mutations were plated together on minimal medium, ***yeastlike*** colonies grew at a frequency of 1 .times. 10-6. These cultures formed mycelia on charcoal agar, confirming the ***presence*** of both mating-type genes. These cells had a single nucleus, as detd. by fluorescence microscopy, and protoplasts had a vol. approx. twice that of protoplasts derived from haploid cells. Flow cytometry of haploid and suspected diploid cells treated with the fluorescent DNA stain propidium iodide showed that the diploids had roughly twice the DNA content of haploid cells. Pulsed field gel electrophoresis confirmed the ***presence*** in the putative diploid cells of chromosomes with unique sizes from both parental haploid strains. Diploids grown under nonselective conditions for 6-23 generations remained stable. Diploid strain W-7 was solopathogenic, i.e., capable of infecting the host when used as the sole inoculum. Sporidia isolated from teliospores from barley infected with strain W-7 contained all possible combinations of auxotrophic markers and mating-type genes. Taken together, these results confirm that stable diploids of U. hordei were formed.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L17 ANSWER 67 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1994:694225 CAPLUS <<LOGINID::20100917>>
DN 121:294225
OREF 121:53655a,53658a
TI ERG10 from Saccharomyces cerevisiae encodes acetoacetyl-CoA thiolase
AU Hiser, Laree; Basson, Michael E.; Rine, Jasper
CS Dep. Molecular Cell Biology, Univ. California, Berkeley, CA, 94720, USA
SO Journal of Biological Chemistry (1994), 269(50), 31383-9
CODEN: JBCHA3; ISSN: 0021-9258
PB American Society for Biochemistry and Molecular Biology
DT Journal
LA English
AB Two recessive alleles of ERG10 and 3 temp.-sensitive recessive alleles of HMG1 (3-hydroxy-3-methylglutaryl-CoA reductase isoenzyme 1) were isolated in a screen for mevalonate ***auxotrophs*** in ***Saccharomyces*** ***cerevisiae*** . The essential, single-copy ERG10 gene was cloned by complementation of the temp.-sensitive phenotype of erg10-21. The 1194-bp continuous open reading frame, encoding a 398-amino acid polypeptide with a calcd. mol. mass of 41,681 daltons, was demonstrated to encode cytoplasmic acetoacetyl-CoA thiolase. Acetoacetyl-CoA thiolase activity corresponded to the no. of copies of ERG10 ***present*** in cell exts., and null alleles of ERG10 produced no detectable acetoacetyl-CoA thiolase enzyme activity. The deduced amino acid sequence was 40-95% identical to acetoacetyl-CoA thiolases from other organisms. This identity included the active site cysteines located at amino acids 91 and 384 in the Erg10 protein.
OSC.G 23 THERE ARE 23 CAPLUS RECORDS THAT CITE THIS RECORD (23 CITINGS)

L17 ANSWER 68 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1994:647402 CAPLUS <<LOGINID::20100917>>
DN 121:247402
OREF 121:44990h,44991a
TI Heterospecific cloning of Arabidopsis thaliana cDNAs by direct complementation of pyrimidine ***auxotrophic*** mutants of ***Saccharomyces*** ***cerevisiae*** . I. Cloning and sequence analysis of two cDNAs catalyzing the second, fifth and sixth steps of the de novo pyrimidine biosynthesis pathway
AU Nasr, Fahd; Bertauche, Nathalie; Dufour, Marie-Elisabeth; Minet, Michele; Lacroute, Francois
CS Cent. Genet. Mol., CNRS, Gif sur Yvette, 91190, Fr.
SO Molecular and General Genetics (1994), 244(1), 23-32
CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB An Arabidopsis thaliana cDNA library was used to complement ***Saccharomyces*** ***cerevisiae*** pyrimidine ***auxotrophic*** mutants. Mutants in all but one (carbamylphosphate synthetase) of the six steps in the de novo pyrimidine biosynthetic pathway could be complemented. The authors report here the cloning, sequencing and computer anal. of two cDNAs encoding the aspartate transcarbamylase (ATCase; EC 2.1.3.2) and orotate phosphoribosyltransferase-orotidine-5'-phosphate decarboxylase (OPRTase-OM-Pdecase; EC 2.4.2.10, EC 4.1.23) enzymes. These results confirm the ***presence*** in A. thaliana of a bifunctional gene whose product catalyzes the last two steps of the pyrimidine biosynthetic pathway, as previously suggested by biochem. studies. The ATCase encoding cDNA sequence (PYRB gene) shows an open reading frame (ORF) of 1173 bp coding for 390 amino acids. The cDNA encoding ORPTase-OMPdecase (PYRE-F gene) shows an ORF of 1431 bp coding for 476 amino acids. Computer anal. of the deduced amino acid sequences of both cDNAs shows the expected high similarity with the ATCase, ornithine transcarbamylase (OTCase; EC 2.1.3.3), OPRTase and OMPdecase families. This heterospecific cloning approach increases our understanding of the genetic organization and interspecific functional conservation of the pyrimidine biosynthetic pathway and underlines its usefulness as a model for evolutionary studies.
OSC.G 15 THERE ARE 15 CAPLUS RECORDS THAT CITE THIS RECORD (15 CITINGS)

L17 ANSWER 69 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1994:597191 CAPLUS <<LOGINID::20100917>>
DN 121:197191
OREF 121:35642h,35643a
TI Molecular analysis of the Trichosporon cutaneum DSM 70698 argG gene and its use for DNA-mediated transformations
AU Reiser, Jakob; Glumoff, Virpi; Ochsner, Urs A.; Fiechter, Armin
CS Inst. Biotechnol., ETH-Honggerberg, Zurich, CH-8093, Switz.
SO Journal of Bacteriology (1994), 176(10), 3012-32 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB Genomic clones capable of complementing a previously isolated arginine ***auxotrophic*** mutant strain of the filamentous ***yeast*** Trichosporon cutaneum DSM 70698 have been identified by DNA-mediated transformation, and a complementing 4,082-bp subfragment was sequenced. This anal. revealed an intact gene (argA) showing a high degree of homol. with the Saccharomyces cerevisiae CPA2 gene encoding the large subunit of carbamoyl-phosphate synthetase (CPS-A). The inferred amino acid sequence of the T. cutaneum argA-encoded protein contains 1,168 residues showing 62% identity with the sequence of the S. cerevisiae CPA2 protein, and the comparison of the two sequences uncovered a putative intron sequence of 81 nucleotides close to the 3' end of the coding region of the T. cutaneum argA gene. The ***presence*** of this intron was confirmed by nuclease protection studies and by direct DNA sequence anal. of a cDNA fragment which had been obtained by PCR amplification. The T. cutaneum intron shares the general characteristics of introns found in yeasts and filamentous fungi. A major transcript of around 4 kb was found in Northern (RNA) blots. The T. cutaneum argA coding region was expressed in Escherichia coli under the control of the regulatable tac promoter. A roughly 130-kDa protein which was found to cross-react with an anti-rat CPS antibody in Western blots (immunoblots) was obsd. Two putative ATP-binding domains were identified, one in the amino-terminal half of the argA-encoded protein and the other in the carboxy-terminal half. These domains are highly conserved among the known CPS-A sequences from S. cerevisiae, E. coli, and the rat. From these results the authors conclude that the T. cutaneum argA gene encodes the large subunit of CPS. This is the first gene to be identified and analyzed in the T. cutaneum DSM 70698 strain.

L17 ANSWER 70 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1994:526498 CAPLUS <<LOGINID::20100917>>
DN 121:126498
OREF 121:22665a,22668a
TI Two radish genes for 3-hydroxy-3-methylglutaryl-CoA reductase isoenzymes complement mevalonate ***auxotrophy*** in a ***yeast*** mutant and yield membrane-bound active enzyme
AU Vollack, Kai Uwe; Dittrich, Baerbel; Ferrer, Albert; Boronat, Albert; Bach, Thomas J.
CS Bot. Inst. II, Univ. Karlsruhe, Karlsruhe, D-76128, Germany
SO Journal of Plant Physiology (1994), 143(4-5), 479-87 CODEN: JPPHEY; ISSN: 0176-1617
DT Journal
LA English
AB Expression of two full-length cDNAs encoding two related isoenzymes of radish (Raphanus sativus L. var. Saxa Knacker) 3-hydroxy-3-methylglutaryl-CoA reductase (HMGR, EC 1.1.1.34) can complement mevalonate ***auxotrophy*** in a ***yeast*** mutant having both HMGR genes (HMG1,HMG2) disrupted [see Basson et al., 1988]. HMGR activity in transformants, placed under the control of the GAL10 promoter, can be induced in the ***presence*** of galactose and is exclusively localized to membranes. Yeast HMGRs contain seven or more membrane-spanning hydrophobic regions, but functional complementation and evidently targeting to yeast membranes shows that the two membrane spans ***present*** in plan HMGRs are already sufficient for membrane insertion.
OSC.G 15 THERE ARE 15 CAPLUS RECORDS THAT CITE THIS RECORD (15 CITINGS)

L17 ANSWER 71 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1994:451277 CAPLUS <<LOGINID::20100917>>
DN 121:51277
OREF 121:9103a,9106a
TI Regulation of THI4 (MOL1), a thiamine-biosynthetic gene of Saccharomyces cerevisiae
AU Praekelt, Uta M.; Byrne, Kerry L.; Meacock, Peter A.
CS 'Leicester Biocent., Univ. Leicester, Leicester, LE1 7RH, UK
SO Yeast (1994), 10(4), 481-90 CODEN: YESTE3; ISSN: 0749-503X
DT Journal
LA English
AB THI4, a Saccharomyces cerevisiae gene originally identified as a result of transient expression in molasses medium and named MOL1 is regulated by thiamine. Using a THI4 promoter-lacZ fusion on a centrometric yeast vector, the authors have shown that the THI4 is completely repressed throughout batch culture by thiamine at a concn. around 1 .mu.M, but shows high level constitutive expression in thiamine-free medium. The transient expression pattern obsd. in molasses medium can be mimicked by the addn. of 0.15 .mu.M-thiamine to defined minimal medium. Cells grown in thiamine-free medium have an intracellular thiamine concn. of around 9 pmol/107 cells. A low level (1 .mu.M) of exogenous thiamine is completely sequestered from the medium within 30 min; intracellular thiamine concns. rise rapidly, followed by a gradual decrease as a result of diln. during growth. A satg. extracellular level of thiamine leads to a maximal intracellular concn. of around 1600 pmol/107 cells, at which point the transport system is shut down. After transfer from repressing to non-repressing medium, THI4 becomes induced when the intracellular concn. of thiamine falls to 20 pmol/107 cells. A thi4::URA3 disruption strain is auxotrophic for thiamine, but can grow in the ***presence*** of hydroxyethyl thiazole, indicating that the gene product is involved in the biosynthetic pathway leading to the formation of the thiazole precursor of thiamine.
OSC.G 52 THERE ARE 52 CAPLUS RECORDS THAT CITE THIS RECORD (52 CITINGS)

L17 ANSWER 72 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1994:212320 CAPLUS <<LOGINID::20100917>>
DN 120:212320
OREF 120:37529a,37532a
TI Auxotrophy-stimulated sensitivity to quaternary ammonium salts and its relation to active transport in yeast
AU Lachowicz, Tadeusz M.; Oblak, Ewa; Piatkowski, Jerzy
CS Inst. Microbiol., Wroclaw Univ., Wroclaw, 94116, Pol.
SO Bulletin of the Polish Academy of Sciences: Biological Sciences (1993), Volume Date 1992, 40(3), 173-82 CODEN: BPABEN; ISSN: 0239-751X
DT Journal

LA English
AB In previous studies the authors have obsd. that ***auxotrophic*** mutants of ***yeast*** were much more sensitive to quaternary ammonium salts than the corresponding isogenic wild-type strains. The supersensitivity of the ***auxotrophs*** seems to be a characteristic feature of ***yeast*** and ***yeast*** -like microorganisms: the level of sensitivity to the quaternary ammonium salts of the bacterial auxotrophs and their original prototrophic forms appeared to be the same. The supersensitivity of ***yeast*** ***auxotrophs*** disappeared on minimal media with ammonium as a nitrogen source. In this report data are ***presented*** that indicate that enrichment of the minimal medium with arginine restores the supersensitivity of ***auxotrophic*** ***yeast*** mutants to the quaternary ammonium salts. The results of amino acid transport into the ***auxotrophic*** ***yeast*** cells treated with a quaternary ammonium salt in the ***presence*** and ***absence*** of arginine are given. A working hypothesis of the mechanism of these salts action as a specific inhibition of nutrient transport is discussed.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)

L17 ANSWER 73 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1994:209833 CAPLUS <<LOGINID::20100917>>
DN 120:209833
OREF 120:37005a,37008a
TI Cloning and nucleotide sequence of a gene conferring ability to grow at a low temperature on ***Saccharomyces*** ***cerevisiae*** tryptophan ***auxotrophs***
AU Kawamura, Daizo; Yamashita, Ichiro; Nimi, Osamu; Tohe, Akio
CS Hiroshima Prefect. Food Technol. Res. Cent., Hiroshima, 732, Japan
SO Journal of Fermentation and Bioengineering (1994), 77(1), 1-9 CODEN: JFBIEX; ISSN: 0922-338X
DT Journal
LA English
AB A gene conferring on yeast YNN140 the ability to grow at a low temp. was cloned and designated LTG3 (low temp. growth gene). Disruption of the LTG3 gene resulted in no growth at a low temp. It was shown that the effect of the ***presence*** of the gene in multicopy was dependent on the strain. DNA sequencing anal. of the LTG3 gene revealed an open reading frame which can encode 592 amino acids. The deduced amino acid sequence of the protein was homologous with that of some amino acid permeases. Since the addn. of a large amt. of L-tryptophan to YPAD medium enabled the YNN140 strain to grow at a low temp., it is possible that a limiting step for YNN140 to grow at a low temp. is to take up tryptophan from the medium. A part of the nucleotide sequence of the cloned DNA contg. the LTG3 gene coincided with that of the SUP3 gene, indicating that the LTG3 gene exists on chromosome XV.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)

L17 ANSWER 74 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1993:642200 CAPLUS <<LOGINID::20100917>>
DN 119:242200
OREF 119:42975a,42978a
TI Screening patients for heterozygous p53 mutations using a functional assay in yeast
AU Ishioka, Chikashi; Frebourg, Thierry; Yan, Yu Xin; Vidal, Marc; Friend, Stephen H.; Schmidt, Susanne; Iggo, Richard
CS Cancer Cent., Massachusetts Gen. Hosp., Charlestown, MA, 02129, USA
SO Nature Genetics (1993), 5(2), 124-9 CODEN: NGENEC; ISSN: 1061-4036
DT Journal
LA English
AB Inherited mutations of the p53 gene significantly increase the risk of developing diverse malignancies, and germline p53 mutations can be detected by assaying the transcriptional activity of the p53 protein in mammalian cells. Here the authors describe a method starting with lymphocytes that allows detection of germline p53 mutations by 'functional' anal. of p53 protein expressed in Saccharomyces cerevisiae. The p53 PCR products are directly cloned into yeast expression vectors in vivo and subsequently ***tested*** for transcriptional activity in a simple growth assay. This technique, functional anal. of sepd. alleles in yeast (FASAY), requires only a few steps, can be automated readily and should permit screening for germline or somatic heterozygous mutations in any gene whose function can be monitored in yeast.
OSC.G 165 THERE ARE 165 CAPLUS RECORDS THAT CITE THIS RECORD (165 CITINGS)

L17 ANSWER 75 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1993:487925 CAPLUS <<LOGINID::20100917>>
DN 119:87925
OREF 119:15633a,15636a
TI General amino acid control regulates MET4, which encodes a methionine-pathway-specific transcriptional activator of Saccharomyces cerevisiae
AU Mountain, Harry A.; Bystroem, Anders S.; Korch, Christopher
CS Dep. Microbiol., Umea Univ., Umea, S-901 87, Swed.
SO Molecular Microbiology (1993), 7(2), 215-28 CODEN: MOMIEE; ISSN: 0950-382X
DT Journal
LA English
AB A met4 mutant of S. cerevisiae was unable to transcribe a no. of genes encoding enzymes of the methionine biosynthetic pathway. The sequence of the cloned MET4 gene allowed the previously sequenced flanking LEU4 and POL1 genes to be linked to MET4 into a 10,327-bp contiguous region of chromosome XIV. From the sequence and mapping of the transcriptional start points, MET4 is predicted to encode a protein of 634 amino acids (as opposed to 666 amino acids published by others) with a leucine zipper domain at the C-terminus, preceded by both acidic and basic regions. Thus, MET4 belongs to the family of basic leucine zipper transactivator proteins. Disruption of MET4 resulted in methionine auxotrophy with no other phenotype. Transcriptional studies showed that MET4 was regulated by general amino acid control and hence by another bZIP protein encoded by GCN4. GCN4 binding sequences are ***present*** between the divergently transcribed MET4 and LEU4 genes. Over-expression of MET4 resulted in leaky expression from the otherwise tightly regulated MET3 promoter under its control. The ***presence*** of consensus sequences for other potential regulatory elements in the MET4 promoter suggests a complex regulation of this gene.
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)

L17 ANSWER 76 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1993:230003 CAPLUS <<LOGINID::20100917>>

DN 118:230003
OREF 118:39687a,39690a
TI Introduction and expression of cDNA encoding Aspergillus oryzae .alpha.-amylase to sake yeast
AU Kimura, Kazuhiro; Kitamoto, Katsuhiko; Gomi, Katsuya; Kumagai, Chieko
CS Natl. Res. Inst. Brew., Tokyo, 114, Japan
SO Nippon Jozo Kyokaishi (1993), 88(3), 233-7 CODEN: NJKYES; ISSN: 0914-7314
DT Journal
LA Japanese
AB A cDNA encoding Aspergillus oryzae .alpha.-amylase was inserted into 3 types of yeast expression vectors. Three types of plasmids, pYTA-1 (YEp type), pRTA-1 (YCp type), and pTAT-11 (YIp type), were introduced to UT-1U, a tryptphan ***auxotrophic*** mutant of sake ***yeast*** . A small scale sake brewing ***test*** carried out using the transformant with pYTA-1 showed that brewing profile was at the same level as that with the parent strain. But UT-1U lost pYTA-1 plasmid during sake brewing. The YEp type plasmid is not stable in cir0 type cells, and Southern blot anal. of UT-1U showed that UT-1U is composed of cir0 type cells. Further more, Southern blot anal. of 7 sake yeast strains showed that all strains are composed of cir0 type cells.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L17 ANSWER 77 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1993:229879 CAPLUS <<LOGINID::20100917>>
DN 118:229879
OREF 118:39659a,39662a
TI Characterization of enzymic synthesis of sphingolipid long-chain bases in ***Saccharomyces*** ***cerevisiae*** : mutant strains exhibiting long-chain-base ***auxotrophy*** are deficient in serine palmitoyltransferase activity
AU Pinto, William J.; Wells, Gerald W.; Lester, Robert L.
CS Coll. Med., Univ. Kentucky, Lexington, KY, 40536, USA
SO Journal of Bacteriology (1992), 174(8), 2575-81 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB Biochem.-genetic anal. of the synthesis of sphingolipid long-chain bases in S. cerevisiae was carried out, and evidence was found for the occurrence of serine palmitoyltransferase (SPT) and 3-ketosphinganine reductase, enzymes that catalyze the initial steps of the pathway in other organisms. SPT activity was demonstrated in vitro with crude membrane prepns. from S. cerevisiae as judged by the formation of radiolabeled 3-ketosphinganine from the condensation of palmitoyl-CoA with radiolabeled serine. Shorter (C12 and C14) and longer (C18) acyl-CoAs sustain significant SPT activity, a result consistent with the finding of both C18 and C20 long-chain bases in the organism. Three products of the long-chain-base synthetic pathway, 3-ketosphinganine, erythrospinganine, and phytosphingosine, neither directly inhibited the reaction in vitro nor affected the specific activity of the enzyme when these bases were included in the culture medium of wild-type cells. Thus, no evidence for either feedback inhibition or repression of enzyme synthesis could be found with these putative effectors. Mutant strains of S. cerevisiae that require a sphingolipid long-chain base for growth fall into 2 genetic complementation groups, LCB1 and LCB2. Membrane prepns. from both lcb1 and lcb2 mutant strains exhibited negligible SPT activity when ***tested*** in vitro. Step 2 of the long-chain-base synthetic pathway was demonstrated by the stereospecific NADPH-dependent redn. of 3-ketosphinganine to erythrosphinganine. Membranes isolated from wild-type cells and from an lcb1 mutant exhibited substantial 3-ketosphinganine reductase activity. Thus, the Lcb- phenotype of these mutants results from a missing or defective SPT, an activity controlled by both the LCB1 and LCB2 genes. These results and earlier work from this lab. establish that SPT plays an essential role in sphingolipid synthesis in S. cerevisiae.
OSC.G 41 THERE ARE 41 CAPLUS RECORDS THAT CITE THIS RECORD (41 CITINGS)

L17 ANSWER 78 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1992:508020 CAPLUS <<LOGINID::20100917>>
DN 117:108020
OREF 117:18757a,18760a
TI Strain improvement of Phaffia rhodozyma by protoplast fusion
AU Chun, Soon Bai; Chin, Jong Eon; Bai, Suk; An, Gil Hwan
CS Coll. Nat. Sci., Chonnam Natl. Univ., Seoul, 500-757, S. Korea
SO FEMS Microbiology Letters (1992), 93(3), 221-6 CODEN: FMLED7; ISSN: 0378-1097
DT Journal
LA English
AB The application of P. rhodozyma as an astaxanthin source in the aquaculture industry is limited because of the low carotenoid content of natural isolates. Carotenoid-hyperproducing hybrids of P. rhodozyma were constructed by protoplast fusion from parental strains that produced approx. 1600 .mu.g carotenoid/g ***yeast*** and were ***auxotrophic*** for tryptophan, leucine, methionine or arginine. The hybrids were stable and consistently produced >2000 .mu.g carotenoid/g yeast. Karyogamy was confirmed by the isolation of recombinants after mitotic segregation of parental auxotrophic genetic markers, the increased content of DNA/cell and the ***presence*** of a single nucleus per cell. The results of this study indicated that protoplast fusion is promising for strain improvement in P. rhodozyma.
OSC.G 19 THERE ARE 19 CAPLUS RECORDS THAT CITE THIS RECORD (19 CITINGS)

L17 ANSWER 79 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1992:466424 CAPLUS <<LOGINID::20100917>>
DN 117:66424
OREF 117:11603a,11606a
TI Sphingolipid long-chain-base ***auxotrophs*** of ***Saccharomyces*** ***cerevisiae*** : genetics, physiology, and a method for their selection
AU Pinto, William J.; Srinivasan, Bharath; Shepherd, Sherri; Schmidt, Ann; Dickson, Robert C.; Lester, Robert L.
CS Coll. Med., Univ. Kentucky, Lexington, KY, 40536, USA
SO Journal of Bacteriology (1992), 174(8), 2565-74 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB A selection method for sphingolipid long-chain-base ***auxotrophs*** of S. ***cerevisiae*** was devised after observing that strains that require a long-chain base for growth become denser when starved for this substance. Genetic anal. of >60 such strains indicated only 2 complementation classes, lcb1 and lcb2. Mutant strains from each class grew equally well with 3-ketodihydrophingosine, erythrodihydrosphingosine or threodihydrosphingosine, or phytosphingosine. Since these metabolites represent the first, second, and last components, resp., of the long-chain-base biosynthetic pathway, it is likely that

the LCB1 and LCB2 genes are involved in the first step of long-chain-based synthesis. The results of long-chain-base starvation in the Lcb- strains suggest that .gtoreq.1 sphingolipids have a vital role in S. cerevisiae. Immediate sequelae of long-chain-base starvation were loss of viability, exacerbated in the ***presence*** of .alpha.-cyclodextrin, and loss of phosphoinositol sphingolipid synthesis but not phosphatidylinositol synthesis. Loss of viability with long-chain-base starvation could be prevented by also blocking either protein or nucleic acid synthesis. Without a long-chain-base, cell division, dry mass accumulation, and protein synthesis continued at a diminished rate and were further inhibited by the detergent Tergitol. The cell d. increase induced by long-chain-base starvation is thus explained as a differential loss of cell division and mass accumulation. Long-chain-base starvation in Lcb- S. cerevisiae and inositol starvation of Inos- S. cerevisiae share common features: an increase in cell d. and a loss of cell viability overcome by blocking macromol. synthesis.
OSC.G 55 THERE ARE 55 CAPLUS RECORDS THAT CITE THIS RECORD (55 CITINGS)

L17 ANSWER 80 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1992:441563 CAPLUS <<LOGINID::20100917>>
DN 117:41563
OREF 117:7243a,7246a
TI Molecular cloning, chromosomal integration, and expression of the homoserine kinase gene THR1 of Saccharomyces cerevisiae
AU Choi, Myoung Sook; Lea, Ho Zoo
CS Dep. Biol., Kangweon Natl. Univ., Chuncheon, 200-701, S. Korea
SO Misaengmul Hakhoechi (1991), 29(1), 16-24 CODEN: MIHCAR; ISSN: 0440-2413
DT Journal
LA English
AB The yeast gene THR1 encodes the homoserine kinase (E.C. 2.7.1.39; HKase) which catalyzes the first step of the threonine-specific arm at the end of the common pathway for methionine and threonine biosynthesis. A recombinant plasmid pMC3 (12.6 kbp, vector YCp50) was cloned into Escherichia coli HB101 from a yeast genomic library through complementation of a thr1 mutation in a yeast recipient strain M39-1D. When subcloned into pMC32 (8.6 kbp, vector YRp7) and pMC35 (8.3 kbp, vector YIp5), the HindIII fragment (2.7 kbp) of the pMC3 insert had thr1-complementing activity in both ***yeast*** and E. coli ***auxotrophic*** strains. The linearized pMC35 was introduced into the original recipient yeast strain and the mitotically stable chromosomal integrant was identified among the transformants. Through tetrad anal., the integration site of the pMC35 was localized to the region of THR1 structural gene at an expected genetic distance of .apprx.11.1 cM from the ARG4 locus on the right arm of the yeast chromosome VIII. When introduced as an episome into the auxotrophic cells and cultured in the ***absence*** of threonine, the cloned gene overexpressed HKase 13-15-fold. HKase levels were repressed by addn. of 300 mg/L and 1190 mg/L threonine for pMC32 and pMC3, resp. Thus, the cloned HindIII yeast DNA fragment contained the yeast THR1 structural gene, along with necessary regulatory components for control of its expression.

L17 ANSWER 81 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1992:189055 CAPLUS <<LOGINID::20100917>>
DN 116:189055
OREF 116:31867a,31870a
TI A dominant mutation that alters the regulation of INO1 expression in Saccharomyces cerevisiae
AU Hosaka, Kohei; Nikawa, Junichi; Kodaki, Tsutomu; Yamashita, Satoshi
CS Sch. Med., Gunma Univ., Maebashi, 371, Japan
SO Journal of Biochemistry (1992), 111(3), 352-8 CODEN: JOBIAO; ISSN: 0021-924X
DT Journal
LA English
AB A dominant, single nuclear gene mutation, CSE1, caused inositol ***auxotrophy*** in ***yeast*** cells. The inositol requirement was marked when choline was ***present*** in the medium. Inositol-1-phosphate synthase, the regulatory enzyme of inositol synthesis, is repressed by inositol, or more profoundly by a combination of inositol and choline in the wild type. In CSE1, the level of inositol-1-phosphate synthase was low and was greatly repressed on the addn. of choline alone. In accordance with this, INO1 mRNA encoding the enzyme was low even under the derepressed conditions and was profoundly decreased by choline in CSE1. But in the wild type, the addn. of choline alone had little effect. An INO1-lacZ fusion was constructed and the control of the INO1 promoter in CSE1 was studied. lacZ Expression was repressed not only by inositol, but also by choline in CSE1, whereas it was repressed by inositol, but only slightly by choline in the wild type. CSE1 Was unlinked to the INO1 structural gene. Thus CSE1 was thought to be a regulatory mutation. Furthermore, when the CDP-choline pathway was mutationally blocked, choline did not affect INO1 expression, indicating that the metab. of choline via the CDP-choline pathway is required for INO1 repression.
OSC.G 16 THERE ARE 16 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)

L17 ANSWER 82 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1992:188859 CAPLUS <<LOGINID::20100917>>
DN 116:188859
OREF 116:31823a,31826a
TI Cloning and characterization of LCB1, a Saccharomyces gene required for biosynthesis of the long-chain base component of sphingolipids
AU Buede, Rebecca; Rinker-Schaffer, Carrie; Pinto, William J.; Lester, Robert L.; Dickson, Robert C.
CS Lucille P. Markey Cancer Cent., Univ. Kentucky, Lexington, KY, 40536, USA
SO Journal of Bacteriology (1991), 173(14), 4325-32 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB The existence of ***auxotrophic*** mutants of S. ***cerevisiae*** having an abs. requirement for the long-chain base (lcb) component of sphingolipids suggests that sphingolipids are crucial for viability and growth. One mutant, termed the lcb1-1 mutant, lacks the activity of serine palmitoyltransferase, the first enzyme in the pathway for long-chain base synthesis. Here, an evidence is ***presented*** that LCB1 has been molecularly cloned. The size of the LCB1 transcript, the direction of transcription, the transcription initiation sites were detd. In addn., the coding region and its 5' and 3' flanking regions were sequenced. Anal. of the DNA sequence revealed a single open reading frame of 1674 nucleotides, encoding a predicted peptide of 558 amino acids. The hydropathy profile of the predicted peptide suggests a hydrophobic, globular, membrane-assocd. protein with two potential transmembrane helices. Comparison of the predicted amino acid sequence to known protein sequences revealed homol. to 5-aminolevulinic acid synthase and

to 2-amino-3-ketobutyrate CoA ligase. These homologies, the similarity of the chem. reactions catalyzed by the 3 enzymes, and the finding that LCB1 restores serine palmitoyltransferase activity to an lcb1-defective strain indicate that serine palmitoyltransferase or a subunit of the enzyme is the most likely product of LCB1. Homol. of the LCB1 predicted protein to the Escherichia coli biotin synthetase was also obsd., but the biol. significance of this observation is not clear. A role for sphingolipid in sporulation is implicated by the finding that diploids homozygous for lch1 failed to sporulate.
OSC.G 108 THERE ARE 108 CAPLUS RECORDS THAT CITE THIS RECORD (108 CITINGS)

L17 ANSWER 83 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1992:145074 CAPLUS <<LOGINID::20100917>>
DN 116:145074
OREF 116:24353a,24356a
TI Cloning of a yeast gene coding for the glutamate synthase small subunit (GUS2) by complementation of ***Saccharomyces*** ***cerevisiae*** and Escherichia coli glutamate ***auxotrophs***
AU Gonzalez, A.; Membrillo-Hernandez, J.; Olivera, H.; Aranda, C.; Macino, G.; Ballario, P.
CS Inst. Fisiol. Cel., UNAM, Mexico City, Mex.
SO Molecular Microbiology (1992), 6(3), 301-8 CODEN: MOMIEE; ISSN: 0950-382X
DT Journal
LA English
AB A S. ***cerevisiae*** glutamate ***auxotroph*** , lacking NADP-glutamate dehydrogenase (NADP-GDH) and glutamate synthase (GOGAT) activities, was complemented with a yeast genomic library. Clones were obtained which still lacked NADP-GDH but showed GOGAT activity. Northern anal. revealed that the DNA fragment ***present*** in the complementing plasmids coded for a 1.5 kb mRNA. Since the only GOGAT enzyme so far purified from S. cerevisiae is made up of a small and a large subunit, the size of the mRNA suggested that the cloned DNA fragment could code for the GOGAT small subunit. Plasmids were purified and used to transform E. coli glutamate auxotrophs. Transformants were only recovered when the recipient strain was an E. coli GDH-less mutant lacking the small GOGAT subunit. These data show that the structural gene coding for the yeast small subunit (GUS2) was cloned. Evidence is also ***presented*** indicating that the GOGAT enzyme which is synthesized in the E. coli transformants is a hybrid comprising the large E. coli subunit and the small S. cerevisiae subunit.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)

L17 ANSWER 84 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1992:80205 CAPLUS <<LOGINID::20100917>>
DN 116:80205
OREF 116:13551a,13554a
TI Effect of ***auxotrophic*** mutation in ***Saccharomyces*** ***cerevisiae*** on the decay of intracellularly accumulated .beta.-lactamase during vegetative growth, encoded on YEp vector
AU Igarashi, Takao; Koide, Kozo; Ohtaguchi, Kazuhisa
CS Fac. Eng., Tokyo Inst. Technol., Tokyo, 152, Japan
SO Biotechnology Letters (1991), 13(11), 815-20 CODEN: BILED3; ISSN: 0141-5492
DT Journal
LA English
AB Using a ura3- and a multi-marked yeast S. cerevisiae strain, both of which carried YEp24, changes in .beta.-lactamase activity per mL of culture were monitored. This enzyme was subject to inactivation depending on the growth phase; its degree was reduced by the ***presence*** of transformant auxotrophy. The auxotroph (host: multi-marked) showed losses and quick recoveries of the activity during the approach to stationary phase, while the prototroph (host: ura3-) less recovery after a dramatic loss. Physiol. heterogeneity between auxotroph and prototroph, evaluated by comparing their growth parameters, might be responsible for such a marked contrast.

L17 ANSWER 85 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1992:57460 CAPLUS <<LOGINID::20100917>>
DN 116:57460
OREF 116:9943a,9946a
TI Optimization of Candida tropicalis cytochrome P450alk gene expression in Saccharomyces cerevisiae with continuous cultures
AU Beretta, Isabella; Sanglard, Dominique; Kaeppeli, Othmar; Fiechter, Armin
CS Inst. Biotechnol., ETH-Honggerberg, Zurich, CH-8093, Switz.
SO Applied Microbiology and Biotechnology (1991), 36(1), 48-60 CODEN: AMBIDG; ISSN: 0175-7598
DT Journal
LA English
AB The cytochrome P450alk gene (P450alk) from C. tropicalis ATCC 750 was expressed in S. cerevisiae CRF18 under control of the alc. dehydrogenase I (ADHI) promoter. To achieve stable expression over long time periods, a 2-.mu.m derived replicative and an integrative expression system were ***tested*** in continuous culture. The 2-.mu.m derived replicative system could not be maintained in cells over high generation nos. In continuous culture, the instability was more pronounced at high diln. rates (D) and high histidine concn., for which the ***yeast*** is ***auxotrophic*** . The nature of the instability was probably due to a gene conversion event between the plasmid and the yeast chromosome. In contrast, the integrative expression system was stably maintained in cells over prolonged cultivation times. Since this work focused on the prodn. of large quantities of P 450 by heterologous expression in yeast over prolonged time periods, the integrant was used to optimize P450alk expression by varying continuous culture parameters. The P450alk expression was dependent on the D applied to the culture. The highest P450alk expression levels were obtained at high D, when cell metab. was shifted to partial glucose oxidn., yielding EtOH as a major metabolite in the culture supernatant. In contrast, when glucose was completely oxidized at low D, the ADHI-dependent P450alk expression was reduced and followed by a corresponding decrease in heterologous protein.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L17 ANSWER 86 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1991:529050 CAPLUS <<LOGINID::20100917>>
DN 115:129050
OREF 115:21981a,21984a
TI Genetic transformation of ***auxotrophic*** mutants of the filamentous ***yeast*** Trichosporon cutaneum using homologous and heterologous marker genes
AU Ochsner, Urs A.; Glumoff, Virpi; Kaelin, Markus; Fiechter, Armin; Reiser, Jakob
CS Inst. Biotechnol., ETH-Hoenggerberg, Zurich, CH-8093, Switz.

SO Yeast (1991), 7(5), 513-24 CODEN: YESTE3; ISSN: 0749-503X
DT Journal
LA English
AB A transformation system for the filamentous ***yeast*** T. cutaneum based on ***auxotrophic*** markers is ***presented*** and techniques for the induction, isolation and characterization of mutants are described. A no. of auxotrophic mutants were isolated and characterized by using biosynthetic precursors and/or inhibitors. A mutant unable to grow in the ***presence*** of ornithine could be complemented successfully in spheroplast transformation expts. using the cloned Aspergillus nidulans ornithine transcarbamoylase gene (argB gene) as selection marker with an efficiency of 5-100 transformants per .mu.g of DNA. In these transformants the heterologous argB gene was ***present*** in multiple tandem copies and the transforming DNA was found to remain stable after more than 50 generations in non-selective media. The same mutant could be complemented by a T. cutaneum cosmid gene library and a complementing cosmid was subsequently isolated from this library by a sib-selection strategy. This cosmid transformed T. cutaneum spheroplasts with an efficiency of 500-200 colonies per .mu.g of DNA. Southern blot anal. were consistent with the view that the transforming sequences became stably integrated into the host genome at the homologous site.

L17 ANSWER 87 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1991:245876 CAPLUS <<LOGINID::20100917>>
DN 114:245876
OREF 114:41497a,41500a
TI Isolation of ***auxotrophic*** mutants. 1. Breeding of wine ***yeasts*** with potent activity to decompose malic acid by protoplast fusion
AU Tachibana, Tadanori; Iwano, Kimio
CS Akita Prefect. Inst. Brew., Akita, 010, Japan
SO Nippon Jozo Kyokaishi (1991), 86(2), 142-6 CODEN: NJKYES; ISSN: 0914-7314
DT Journal
LA Japanese
AB ***Auxotrophic*** mutants were obtained from Schizosaccharomyces pombe p-1011 and ***Saccharomyces*** ***cerevisiae*** Kyokai-1 for breeding yeasts with high ability of decompg. malic acid and with good flavor by protoplast fusion for prodn. of plum wine. After UV irradn., 49 auxotrophic mutants were selected by nystatin treatment. Plum juice was fermented with these mutants for 3 days at 30.degree. to examine decompn. of malic acid, sensory ***test*** , fermn. rate, and specific growth rate. Two strains were selected as candidates for protoplast fusion: uracil ***auxotroph*** E-1 from S. ***cerevisiae*** Kyokai-1 and arginine ***auxotroph*** C-6 from S. pombe p-1011.

L17 ANSWER 88 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1990:568901 CAPLUS <<LOGINID::20100917>>
DN 113:168901
OREF 113:28594h,28595a
TI Quantification of physical and cytophysiological conditions for the electrofusion of Saccharomyces cerevisiae
AU Noda, Kotaro; Togawa, Yoshiyuki; Yamada, Yasuyuki
CS Biotechnol. Instrum. Dep., Shimadzu Corp., Kyoto, 604, Japan
SO Agricultural and Biological Chemistry (1990), 54(8), 2023-8 CODEN: ABCHA6; ISSN: 0002-1369
DT Journal
LA English
AB Various conditions for obtaining hybrids of the ***auxotrophic*** mutants SH1509 and SH1512 of S. ***cerevisiae*** by electrofusion were investigated. An AC field of 400 Vp/cm and a DC field of 2 squares pulses (7 kV/cm; 60 .mu.sec each) at an interval of 0.5 s were effective. Treatment with 0.2 (SH1509) or 1.0 mg/mL (SH1512) Zymolyase for 1 or 1.5 h was essential. The hybrid yield peaked at 0.6M sorbitol as osmotic stabilizer. The ***presence*** of CaCl2 (.ltoreq.0.4 mM) or 0.1 mM CaCl2 with 0.1 mM MgCl2 enhanced the yield. The temp. of the spheroplast suspension during pulsations also affected the yield, the most suitable temp. being 28.degree..
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L17 ANSWER 89 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1990:472240 CAPLUS <<LOGINID::20100917>>
DN 113:72240
OREF 113:12093a,12096a
TI Characterization of a leuA gene and an ARS element from Mucor circinelloides
AU Roncero, M. Isabel G.; Jepsen, Lars Peter; Stroeman, Per; Van Heeswijck, Robyn
CS Dep. Physiol., Carlsberg Lab., Copenhagen, DK-2500, Den.
SO Gene (1989), 84(2), 335-43 CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB A 4.4-kb PstI restriction endonuclease fragment of M. circinelloides DNA has previously been shown to both complement a leuA- mutation, and to enable the autonomous replication of plasmids within this organism. The complete nucleotide (nt) sequence of this fragment was detd. and an open reading frame of 1935 bp with no introns was identified, which exhibits significant similarity [75% at the nucleotide (nt) level] with 114 bp of the 5'-coding region of the Saccharomyces cerevisiae LEU1 gene. Based on this and on the fact that the fragment weakly complements a leu1 ***auxotroph*** of S. ***cerevisiae*** , it was concluded that the Mucor leu gene encodes .alpha.-isopropylmalate (.alpha.-IPM) isomerase and designated it leuA+ accordingly. Primer extension anal. of leuA mRNA and Northern-blot hybridization, showed that the leuA transcript is .apprxeq.2.3 kb, with 5'- and 3'-untranslated regions of 16-20 nt and .apprxeq.450 nt, resp. Specific Mucor ARS sequence(s) were not identified, although the general location of ARS was indicated by subcloning expts. Nucleotide sequences are ***present*** within this region, which show some similarity with the core consensus of the S. cerevisiae ARS; however, any functional homol. is doubtful, since insertion of the 4.4-kb PstI fragment into YIp5 did not increase the transformation frequency of S. cerevisiae with such a vector.
OSC.G 36 THERE ARE 36 CAPLUS RECORDS THAT CITE THIS RECORD (36 CITINGS)

L17 ANSWER 90 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1990:438841 CAPLUS <<LOGINID::20100917>>
DN 113:38841
OREF 113:6601a,6604a
TI Lipid production of revertants of Ufa mutants from the oleaginous yeast Apiotrichum curvatum
AU Ykema, Adrie; Verbree, Elizabeth C.; Verwoert, Ira I. G. S.; Van der Linden, Karin H.; Nijkamp, H. John J.; Smit, Henk

CS Dep. Genet., Vrije Univ., Amsterdam, 1081 HV, Neth.
SO Applied Microbiology and Biotechnology (1990), 33(2), 176-82 CODEN: AMBIDG; ISSN: 0175-7598
DT Journal
LA English
AB From six unsatd. fatty acid ***auxotrophs*** (Ufa mutants) of the oleaginous ***yeast*** A. curvatum blocked in the conversion of stearic to oleic acid, were isolated revertants able to grow in the ***absence*** of unsatd. fatty acids, in a search for strains that can produce cocoa butter equiv. A broad range in the percentage of satd. fatty acids (% SFA) was obsd. in the lipids of individual revertants (varying from 27-86% SFA), compared with the wild-type (44% SFA). Further anal. of fatty acid compn. indicated that: (i) not all 6 Ufa mutants had the same genetic background and (ii) one specific Ufa mutation could be reverted in more than one way. Revertants that produced lipids with >50% SFA where examd. further. These strains were cultivated for 50 generations and half of them produced lipids with high % SFA after that time and were defined as stable. The viability of revertant strains with extremely high % SFA (>80%) may be explained by the finding that polar lipids, which are part of yeast membranes, contained much more polyunsatd. fatty acids and a significant lower % SFA than neutral (storage) lipids. One revertant (R25.75) was selected that was able to produce lipids in whey permeate at a rate comparable with wild-type A. curvatum and with a fatty acid compn. and congelation curve comparable with cocoa butter.
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)

L17 ANSWER 91 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1990:96930 CAPLUS <<LOGINID::20100917>>
DN 112:96930
OREF 112:16479a,16482a
TI Isolation and characterization of fatty acid ***auxotrophs*** from the oleaginous ***yeast*** Apiotrichum curvatum
AU Ykema, Adrie; Verbree, Elizabeth C.; Nijkamp, H. John J.; Smit, Henk
CS Dep. Genet., Vrije Univ., Amsterdam, 1081 HV, Neth.
SO Applied Microbiology and Biotechnology (1989), 32(1), 76-84 CODEN: AMBIDG; ISSN: 0175-7598
DT Journal
LA English
AB In order to improve the economic value of lipids produced by A. curvatum ATCC 20509, a search was made for mutants defective in the conversion of stearic acid to oleic acid. Mutants could be selected as unsatd. fatty acid auxotrophs, since unsatd. fatty acids are essential components in membrane lipids. After treatment of A. curvatum wild-type with N-methyl-N'-nitro-N'-nitrosoguanidine, 58 fatty-acid-requiring mutants were isolated. On the basis of the growth response to satd. and unsatd. fatty acids and the fatty acid compn. of lipids produced by these mutants, it was concluded that only 18 were real unsatd. fatty acid mutants, while the other 40 were designated as fatty acid synthetase mutants. The former mutants of A. curvatum are able to produce high amts. of lipids consisting of >90% triacylglycerols with a percentage of satd. fatty acids resembling that of cocoa butter, when grown in the ***presence*** of relatively small amts. of oleic acid in the growth medium. This may offer an economically favorable alternative for the prodn. of cocoa butter equivs. by microorganisms.
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L17 ANSWER 92 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1990:4231 CAPLUS <<LOGINID::20100917>>
DN 112:4231
OREF 112:843a,846a
TI Structural discrimination in the sparking function of sterols in the yeast Saccharomyces cerevisiae
AU Lorenz, R. Todd; Casey, Warren M.; Parks, Leo W.
CS Dep. Microbiol., North Carolina State Univ., Raleigh, NC, 27695, USA
SO Journal of Bacteriology (1989), 171(11), 6169-73 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB A S. ***cerevisiae*** sterol ***auxotroph*** , SPK14 (a hem1 erg6 erg7 ura), was constructed to ***test*** the ability of selected C-5,6 unsatd. sterols at growth-limiting concns. to spark growth on bulk cholestanol.. The native sterol, ergosterol, initiated growth faster and allowed a greater cell yield than did other sterols selectively altered in one or more features of the sterol. Although the C-5,6 unsatn. is required for the sparking function, the ***presence*** of the C-22 unsatn. facilitated sparking far better than did the C-7 unsatn., whereas the C-24 Me was the least important group. The addn. of .delta.-aminolevulinic acid to the medium allowed the sparking of FY3 (hem1 erg7 ura) on bulk cholestanol due to the derepression of 3-hydroxy-3-methylglutaryl-CoA reductase and the prodn. of endogenous ergosterol. The optimal concn. of .delta.-aminolevulinic acid to spark growth was 800 ng/mL, whereas higher concns. caused a growth inhibition. The growth yield of FY3 reached a plateau max. at .apprx.5 .mu.g/mL when the bulk cholestanol was varied in the ***presence*** of 10 ng sparking ergosterol/mL.
OSC.G 20 THERE ARE 20 CAPLUS RECORDS THAT CITE THIS RECORD (20 CITINGS)

L17 ANSWER 93 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1989:570834 CAPLUS <<LOGINID::20100917>>
DN 111:170834
OREF 111:28373a,28376a
TI Regulation by heme of sterol uptake in Saccharomyces cerevisiae
AU Shinabarger, Dean L.; Keesler, George A.; Parks, Leo W.
CS Dep. Microbiol., North Carolina State Univ., Raleigh, NC, 27695-7615, USA
SO Steroids (1989), 53(3-5), 607-23 CODEN: STEDAM; ISSN: 0039-128X
DT Journal
LA English
AB The leaky heme mutants G204, G216, and G214 are shown to accumulate exogenous sterols. Unlike hem mutants which have complete blocks in the heme pathway, these strains do not require ergosterol, methionine, or unsatd. fatty acids for growth. The addn. of aminolevulinic acid to the growth medium inhibited sterol uptake in G204 96% but had only a slight effect on sterol uptake by strains G214 and G216. Sterol uptake in all 3 strains was inhibited 83-94% when cells were grown in the ***presence*** of hematin. Sterol anal. of these strains grown in the ***presence*** and ***absence*** of either aminolevulinic acid or hematin revealed that satn. of the cell membrane with ergosterol was not responsible for the dramatic decrease in sterol uptake. These results suggest that sterol uptake by yeast cells is controlled by heme, and explain the nonviability of ***yeast*** strains that are heme competent and ***auxotrophic*** for sterols.

OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)

L17 ANSWER 94 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1989:474681 CAPLUS <<LOGINID::20100917>>
DN 111:74681
OREF 111:12519a,12522a
TI Inhibition of DNA synthesis in Saccharomyces cerevisiae by yeast killer toxin KT28
AU Schmitt, Manfred; Brendel, Martin; Schwarz, Ralf; Radler, Ferdinand
CS Inst. Mikrobiol. Weinforsch., Johannes Gutenberg-Univ., Mainz, D-6500, Fed. Rep. Ger.
SO Journal of General Microbiology (1989), 135(6), 1529-35 CODEN: JGMIAN; ISSN: 0022-1287
DT Journal
LA English
AB Treatment of sensitive cells of S. cerevisiae with killer toxin KT28 affected cell viability after 2 h; the effect was dependent upon the availability of a utilizable energy source. Treatment led to an interruption of cell growth. The mother cells contained nuclear DNA, whereas their daughter buds did not. Using a killer-toxin-sensitive thymidine ***auxotroph*** of S. ***cerevisiae*** carrying a temp.-sensitive thymidylate uptake mutation, it was shown that the incorporation of dTMP at the permissive temp. was inhibited within 30 min of the addn. of KT28. When cells labeled at the permissive temp. were incubated at the restrictive temp., the level of radioactivity declined in the ***absence*** but not in the ***presence*** of KT28. No other effects of KT28 were obsd. within 2 h of its addn., and it is concluded that the inhibition of DNA synthesis is an early effect of the action of KT28.
OSC.G 12 THERE ARE 12 CAPLUS RECORDS THAT CITE THIS RECORD (12 CITINGS)

L17 ANSWER 95 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1989:228321 CAPLUS <<LOGINID::20100917>>
DN 110:228321
OREF 110:37783a,37786a
TI Polyamines, macromolecular synthesis and ribosomes in Saccharomyces cerevisiae
AU Miret, J. J.; Goldemberg, Sara H.
CS Inst. Invest. Bioquim. "Fundacion Campomar", Buenos Aires, 1405, Argent.
SO Yeast (1989), 5(Spec. Issue), S333-S337 CODEN: YESTE3; ISSN: 0749-503X
DT Journal
LA English
AB Expts. with a polyamine ***auxotrophic*** strain of S. ***cerevisiae*** showed, as in bacterial system (Escherichia coli), reduced synthesis of macromols. (DNA, RNA, and protein) and an abnormal ribosomal assocn. pattern in polyamine-depleted yeast cells. These findings indicate that lack of polyamines affects ribosome organization not only in prokaryotes but also in some eukaryotic cells. Depletion of polyamines appeared to affect yeast cell walls too, making them partially resistant to enzymic lysis by zymolyase, which completely attacked them when the cells were cultivated in the ***presence*** of polyamine.

L17 ANSWER 96 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1989:54316 CAPLUS <<LOGINID::20100917>>
DN 110:54316
OREF 110:8917a,8920a
TI Evidence for cooperation between cells during sporulation of the yeast Saccharomyces cerevisiae
AU Jakubowski, Hieronim; Goldman, Emanuel
CS New Jersey Med. Sch., UMDNJ, Newark, NJ, 07103, USA
SO Molecular and Cellular Biology (1988), 8(12), 5166-78 CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB Diploid S. cerevisiae cells heterozygous for the mating type locus (MATa/MAT.alpha.) undergo meiosis and sporulation when starved for nitrogen in the ***presence*** of a poor carbon source such as potassium acetate. Diploid ***yeast*** adenine ***auxotrophs*** sporulated well at high cell d. (107 cells/mL) under these conditions but failed to differentiate at low cell d. (105 cell/mL). The conditional sporulation-deficient phenotype of adenine ***auxotrophs*** could be complemented by wild-type ***yeast*** cells, by medium from cultures that sporulate at high d., or by exogenously added adenine (or hypoxanthine with some mutants). Adenine and hypoxanthine in addn. to guanine, adenosine, and numerous nucleotides were secreted into the medium, each in its unique temporal pattern, by sporulating ***auxotrophic*** and prototrophic ***yeast*** strains. The major sourced of these compds. was degrdn. of RNA. The data indicated that differentiating yeast cells cooperate during sporulation in maintaining sufficiently high concns. of extracellular purines which are absolutely required for sporulation of adenine auxotrophs. Yeast prototrophs, which also sporulated less efficiently at low cell d. (106 cells/mL), reutilized secreted purines in preference to de novo-made purine nucleotides whose synthesis was in fact inhibited during sporulation at high cell d. Adenine enhanced sporulation of yeast prototrophs at low d. The behavior of adenine auxotrophs bearing addnl. mutations in purine salvage pathways genes (ade apt1, ade aah1 apt1, ade hpt1) supports a model in which secretion of degrdn. products, uptake, and reutilization of these products is a signal between cells synchronizing the sporulation process.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)

L17 ANSWER 97 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1989:36580 CAPLUS <<LOGINID::20100917>>
DN 110:36580
OREF 110:6045a,6048a
TI Lysine biosynthesis pathway and biochemical blocks of lysine auxotrophs of Schizosaccharomyces pombe
AU Ye, Zhi Hai; Bhattacharjee, J. K.
CS Dep. Microbiol., Miami Univ., Oxford, OH, 45056, USA
SO Journal of Bacteriology (1988), 170(12), 5968-70 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB The .alpha.-aminoadipate (AA) pathway for the biosynthesis of lysine was investigated in the wild type and in lysine ***auxotrophs*** of the fission ***yeast*** S. pombe. Of the 8 enzyme activities of the AA pathway that have been examd. so far, 6 were ***present*** in the ext. of wild-type S. pombe cells. Growth response to AA and accumulation studies indicated that 3 lysine auxotrophs, the lys2-97, lys4-95, and lys8-1 strains were blocked before the AA step and that 4 lysine auxotrophs, the lys1-131, lys3-37, lys6-3, and lys7-2 strains, were blocked after the AA step. The lys2-97 mutant exhibited an enzyme lesion at the cis-homoaconitate hydratase step, the lys1-131 and lys7-2 mutants exhibited lesions at the AA reductase step, and

lys3-37 exhibited a lesion at the saccharopine dehydrogenase step. These results demonstrated the basic similarity of the AA pathway in S. pombe and Saccharomyces cerevisiae.
OSC.G 18 THERE ARE 18 CAPLUS RECORDS THAT CITE THIS RECORD (18 CITINGS)

L17 ANSWER 98 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1988:546084 CAPLUS <<LOGINID::20100917>>
DN 109:146084
OREF 109:24219a,24222a
TI Genetic and molecular characterization of a distillers' yeast
AU Keiding, Kristine
CS Dep. Physiol., Carlsberg Lab., Copenhagen Valby, 2500, Den.
SO Foundation for Biotechnical and Industrial Fermentation Research, [Publication] (1987), 5(Ind. Yeast Genet.), 159-76
CODEN: FBIREN; ISSN: 0780-6655
DT Journal
LA English
AB A distillers prodn. Saccharomyces cerevisiae yeast strain, strain A, can be sporulated and microdissected. Spore viability is 40%. From 4 dissected asci, all 4 spores in each ascus were viable. Auxotrophic mutants have been induced in meiotic segregants of strain A by UV irradn. and EMS treatment. Two spore-derived strains of strain A, A91 and A209, were crossed to haploid S. ***cerevisiae*** strains carrying several ***auxotrophic*** markers. Tetrad anal. of the mating products revealed that A91 and A209 are disomic for 6 and 7 chromosomes, resp., out of 7 chromosomes investigated, i.e. they are essentially diploid. Chromosomes III from strain A were compared to their counterparts in std. strains of S. cerevisiae at several loci by hybridization of chromosomal DNA to cloned DNA from HIS4, LEU2, and MAT loci from S. cerevisiae. Four different chromosomes III in the distillers' strain were identified. Of the four chromosomes, 3 were lacking HML and one was lacking HMR. Furthermore, of the 4 MAT genes, 2 were MATa, one was mata and 1 was MAT.alpha.. These data are consistent with the assumption that all loci ***tested*** are organized in the same order as in the genetically analyzed std. strains. Thus, strain A, may be tetraploid.

L17 ANSWER 99 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1988:546025 CAPLUS <<LOGINID::20100917>>
DN 109:146025
OREF 109:24207a,24210a
TI Inhibition of sterol synthesis by .DELTA.5-sterols in a sterol ***auxotroph*** of ***yeast*** defective in oxidosqualene cyclase and cytochrome P-450
AU Nes, William R.; Dhanuka, Inder C.
CS Dep. Biosci. Biotechnol., Drexel Univ., Philadelphia, PA, 19104, USA
SO Journal of Biological Chemistry (1988), 263(24), 11844-50
CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB Synthesis of ergosterol is demonstrated in the GL7 mutant of Saccharomyces cerevisiae. This sterol auxotroph has been thought to lack the ability to synthesize sterols due both to the ***absence*** of 2,3-oxidosqualene cyclase and to a heme deficiency eliminating cytochrome P 450 which is required in demethylation at C-14. However, when the medium sterol was 5.alpha.-cholestan-3.beta.-ol, 5.alpha.-cholest-8(14)-en-3.beta.-36, or 24.beta.-methyl-5.alpha.-cholest-8(14)-en-3.beta.-ol, sterol synthesis was found to proceed yielding 1-3 fg/cell of ergosterol (24.beta.-methylcholesta-5,7,22E-trien-3.beta.-ol). Ergosterol was identified by mass spectroscopy, gas and high performance liq. chromatog., UV spectroscopy, and radioactive labeling from [3H]acetate. Except for some cholest-5-en-3.beta.-ol (cholesterol) which was derived from the 5.alpha.-cholestan-3.beta.-ol, the stanol and the two 8(14)-stenols were not significantly metabolized, confirming the ***absence*** of an isomerase for migration of the double bond from C-8(14) to C-7. Drastic redn. of ergosterol synthesis to not more than 0.06 fg/cell was obsd. when the medium sterol either had a double bond at C-5, as in the case of cholesterol, or could be metabolized to a sterol with such a bond. Thus, both 5.alpha.-cholest-8(9)-en-3.beta.-ol and 5.alpha.-cholest-7-en-3.beta.-ol (lathosterol) were converted to cholesta-5,7-dien-3.beta.-ol (7-dehydrocholesterol), and the ***presence*** of the latter dienol depressed the level of ergosterol. The most attractive of the possible explanations for these observations is the assumption of two genetic compartments for synthesis of sterols, one of which has and one of which has not been affected by the two mutations. The ability, despite the mutations, to synthesize small amts. of ergosterol which could act to regulate the cell cycle may also explain why this mutant can grow aerobically with cholesterol (acting in the bulk membrane role) as the sole exogenous sterol.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)

L17 ANSWER 100 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1988:450038 CAPLUS <<LOGINID::20100917>>
DN 109:50038
OREF 109:8339a,8342a
TI Metabolic fate of N'-methyladenine in ***yeast*** ***auxotrophic*** to adenine
AU Murthy, M. S. S.; Deorukhakar, V. V.
CS Div. Radiol. Protect., Bhabha At. Res. Cent., Bombay, 400 085, India
SO Mutation Research Letters (1988), 208(1), 51-6 CODEN: MRLEDH; ISSN: 0165-7992
DT Journal
LA English
AB The metabolic fate of N1-methyladenine in yeast with respect to its incorporation into RNA was studied. Chromatog. anal. of the PCA-sol. and -insol. fractions of cells grown in the combined ***presence*** of adenine and 3H-labeled N1-methyladenine show that (a) N1-methyladenine can enter the cells, (b) however, it is very poorly utilized by the salvage pathway for nucleic acid synthesis, and (c) the inhibition occurs probably at the 1st stage of conversion of the methylated base to the corresponding nucleotide.

L17 ANSWER 101 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1988:434094 CAPLUS <<LOGINID::20100917>>
DN 109:34094
OREF 109:5701a,5704a
TI Studies on a lectin from Saccharomyces cerevisiae
AU Kundu, Manikuntala; Basu, Joyoti; Chakrabarti, Parul
CS Dep. Chem., Bose Inst., Calcutta, 700 009, India
SO Indian Journal of Biochemistry & Biophysics (1988), 25(1-2), 204-8 CODEN: IJBBBQ; ISSN: 0301-1208
DT Journal
LA English
AB The effect of chem. modification on a galactose-specific lectin isolated from a fatty acid ***auxotroph*** of S. ***cerevisiae*** was investigated in order to know the type of amino acids involved in its agglutinating activity. Modification of 50 free amino groups with succinic anhydride or citraconic

anhydride led to an almost complete loss of activity. This could not be prevented by the inhibitory sugar Me .alpha.-D-galactopyranoside. Treatment with N-bromosuccinimide and N-acetylimidazole, for the modification of tryptophan and tyrosine residues, did not affect lectin activity. Modification of carboxy groups with glycine Et ester greatly affected lectin activity, although sugars afforded partial protection against this. Modification of 4 thiol groups with N-ethylmaleimide was accompanied by a loss of 85% of the agglutinating activity, and 2 thiol groups were ***present*** at the sugar-binding site of the lectin. Modification of 18 arginine residues with cyclohexane-1,2-dione and 26 histidine residues with ethoxyformic anhydride led to a loss of lectin activity. However, in these cases, modification was not protected by the above mentioned inhibitory sugar, suggesting the ***absence*** of these groups at the sugar-binding site. The lectin was nonmitogenic toward human lymphocytes and contained 2 binding sites for lactose.

L17 ANSWER 102 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1988:144532 CAPLUS <<LOGINID::20100917>>
DN 108:144532
OREF 108:23599a,23602a
TI Isolation of the yeast INO4 gene, a positive regulator of phospholipid biosynthesis
AU Klig, Lisa S.; Hoshizaki, Deborah K.; Henry, Susan A.
CS Dep. Genet. Mol. Biol., Albert Einstein Coll. Med., Bronx, NY, 10461, USA
SO Current Genetics (1988), 13(1), 7-14 CODEN: CUGED5; ISSN: 0172-8083
DT Journal
LA English
AB ***Yeast*** ino4 mutants are ***auxotrophic*** for the phospholipid precursor inositol and have pleiotropic defects in phospholipid synthesis. The mutants are unable to derepress the cytoplasmic enzyme, inositol-1-phosphate synthase and they exhibit reduced synthesis of methylated phospholipids, particularly phosphatidylcholine. The INO4 gene is believed to encode a pos. regulator involved in coordinate control of phospholipid synthesis. In the ***present*** study, the isolation of two clones contg. the INO4 gene is reported. The clones share a region of homol. and were mapped to the INO4 locus. Southern blot anal. revealed that the cloned DNA contained both unique and repetitive DNA.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)

L17 ANSWER 103 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1988:109393 CAPLUS <<LOGINID::20100917>>
DN 108:109393
OREF 108:17859a,17862a
TI Use of intergeneric fusions to identify mutations in the asporogenous yeast Candida tropicals
AU Golovina, G. I.; Solov'eva, I. M.; Zolotarev, F. N.; Domkin, V. D.; Alenin, V. V.
CS Ob'ed. "Gidrolizprom", LGU, Leningrad, USSR
SO Molekulyarnaya Genetika, Mikrobiologiya i Virusologiya (1988), (1), 29-33 CODEN: MGMVDU; ISSN: 0208-0613
DT Journal
LA Russian
AB The possibility of genetic identification of mutations in an asporogenous yeast by the technique of intergeneric fusion of protoplasts of Candida tropicalis and Saccharomyces cerevisiae was demonstrated for C. tropicalis strains G5-9 (Ade- Leu-) and G32-4 (Leu-). The mutations to Ade- auxotrophy in strain G5-9 and to Leu- auxotrophy in strain G32-4 of C. tropicalis are allelic to ade2 and leu1 genes of S. cerevisiae. The allelic character of the Ade- ***auxotrophy*** mutation in C. tropicalis and the ade2 gene of S. ***cerevisiae*** is confirmed by the ***absence*** of AIR-carboxylase activity in a cellular ext. from strain G5-9.

L17 ANSWER 104 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1987:549972 CAPLUS <<LOGINID::20100917>>
DN 107:149972
OREF 107:24053a,24056a
TI Partial purification and some properties of homoserine O-acetyltransferase of a methionine ***auxotroph*** of ***Saccharomyces*** ***cerevisiae***
AU Yamagata, Shuzo
CS Fac. Gen. Educ., Gifu Univ., Gifu, 501-11, Japan
SO Journal of Bacteriology (1987), 169(8), 3458-63 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB A wild-type strain and 6 methionine ***auxotrophs*** of S. ***cerevisiae*** were cultured in a synthetic medium supplemented with 0.1 mM L-cysteine or L-methionine and analyzed for the synthesis of homoserine O-acetyltransferase (EC 2.3.1.31). Among them, 4 mutant strains exhibited enzyme activity in cell exts. Methionine added to the synthetic medium at concns. >0.1 mM repressed enzyme synthesis in 2 of these strains. The enzyme was partially purified (3500-fold) from an ext. of a mutant strain through (NH4)2SO4 fractionation and chromatog. on columns of DEAE-cellulose, Phenyl-Sepharose CI-4B, and Sephadex G-150. The enzyme exhibited optimal pH at 7.5 for activity and at 7.8 for stability. The reaction product was O-acetyl-L-homoserine, confirming that it produced L-homocysteine in an O-acetyl-L-homoserine sulfhydrylase reaction. The Km for L-homoserine was 1.0 mM, and for Ac CoA it was 0.027 mM. The mol. wt. of the enzyme was estd. to be .apprx.104,000 by Sephadex G-150 column chromatog. and 101,000 by sucrose d. gradient centrifugation. The isoelec. point was at pH 4.0. Of the hydroxy amino acids examd., the enzyme showed reactivity only to L-homoserine. Succinyl CoA was not an acyl donor. In the ***absence*** of L-homoserine, Ac CoA was deacylated by the enzyme, with a Km of 0.012 mM. S-Adenosylmethionine and S-adenosylhomocysteine slightly inhibited the enzyme, but methionine had no effect.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)

L17 ANSWER 105 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1987:453310 CAPLUS <<LOGINID::20100917>>
DN 107:53310
OREF 107:8763a,8766a
TI The mapping of chromosomes in Saccharomyces cerevisiae. I. A cosmid vector designed to establish, by cloning into cdc-mutants, numerous start loci for chromosome walking in the yeast genome
AU Breter, Hans Joachim; Knoop, Marie Theres; Kirchen, Heinz
CS Physiol.-Chem. Inst., Johannes Gutenberg-Univ., Mainz, D-6500, Fed. Rep. Ger.
SO Gene (1987), 53(2-3), 181-90 CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB A series of vectors for cosmid cloning in yeast was derived from cosmid pHC79. Vectors pMT4 through pMT6 contain 2

tandemly arranged cohesive end sites (cos) from the genome of bacteriophage .lambda.. Their design allows the rapid and simple prepn. of cosmid arms by linearizing a vector at the unique PvuII restriction site located between the 2 cos sequences and then cutting the linearized mol. at one of its unique cloning sites for BamHI, ClaI, PvuI, SalI, or ScaI. Cosmids generated with arms from the most advanced vector, pMT6, carry the origin of replication (ori) and the ampicillin-resistance gene from pBR322 and the TRP1/ARS1 and URA1 genes from S. cervisiae. A yeast genomic DNA library was established by packaging in vitro, into phage .lambda. preheads, of partially restricted yeast DNA fragments ligated to cosmid arms of vector pMT6. About 80% of the clones thus obtained comprise inserts of contiguous genomic DNA >30 kb in length. Unique DNA probes for the yeast genes CDC10, CDC36, HIS4, LEU2, and PGK1 have successfully been applied when ***testing*** for completeness of this library by isolating a series of overlapping cosmid clones that carry the resp. genes. The library will thus be useful for the selection of cosmid clones which carry CDC genes from yeast by complementing first, with the vectorial ***yeast*** gene URA1, the pyrimidine ***auxotrophy*** of most cdc strains and then, with the resp. CDC wild-type genes, of the temp.-sensitive mutant alleles. Most CDC clones thus obtained will provide unique DNA probes which serve as randomly distributed start sequences within the yeast genome for overlap hybridization screening in chromosome mapping studies.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L17 ANSWER 106 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1987:435351 CAPLUS <<LOGINID::20100917>>
DN 107:35351
OREF 107:5843a,5846a
TI Chemical modification studies on a lectin from Saccharomyces cerevisiae (bakers' yeast)
AU Kundu, Manikuntala; Basu, Joyoti; Ghosh, Amitabha; Chakrabarti, Parul
CS Dep. Chem., Bose Inst., Calcutta, 700 009, India
SO Biochemical Journal (1987), 244(3), 579-84 CODEN: BIJOAK; ISSN: 0306-3275
DT Journal
LA English
AB The effect of chem. modification on a galactose-specific lectin isolated from a fatty acid ***auxotroph*** of S. ***cerevisiae*** was investigated in order to identify the type of amino acids involved in its agglutinating activity. Modification of 50 free amino groups with succinic anhydride or citraconic anhydride led to an almost complete loss of activity. This was not protected by the inhibitory sugar Me .alpha.-D-galactopyranoside. Treatment with N-bromosuccinimide and N-acetylimidazole, for the modification of tryptophan and tyrosine residues, did not affect lectin activity. Modification of carboxy groups with glycine Et ester greatly affected lectin activity, although sugars afford partial protection. Modification of 4 SH groups with N-ethylmaleimide was accompanied by a loss of 85% of the agglutinating activity, and 2 SH groups were found to be ***present*** at the sugar-binding site of the lectin. Modification of 18 arginine residues with cyclohexane-1,2-dione and 26 histidine residues with ethoxyformic anhydride led to a loss of lectin activity. However, in these cases, modification was not protected by the above mentioned inhibitory sugar, suggesting the ***absence*** of these groups at the sugar-binding site. In all the cases, immunodiffusion studies with modified lectin showed no gross structural changes which could disrupt antigenic sites of the lectin.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L17 ANSWER 107 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1987:210811 CAPLUS <<LOGINID::20100917>>
DN 106:210811
OREF 106:34133a,34136a
TI Base analog mutagenesis in yeast and its modulation by pyrimidine deoxynucleotide pool imbalances: incorporation of bromodeoxyuridylate and iododeoxyuridylate
AU Ross, Linda S.; Landman, Orna; Little, J. G.
CS Dep. Biol., York Univ., Toronto, ON, M3J 1P3, Can.
SO Current Genetics (1987), 11(6-7), 421-7 CODEN: CUGED5; ISSN: 0172-8083
DT Journal
LA English
AB Cells of the ***yeast*** , ***Saccharomyces*** ***cerevisiae*** , which are ***auxotrophic*** for thymidylate (tmp1) can also incorporate analogs of thymidylate. When the base analog, 5-bromodeoxyuridylate, is incorporated into tmp1 yeast cells it is lethal and mutagenic. Both lethality and mutation induction can be drastically altered by perturbation of the pyrimidine nucleotide pools. Anal. of mutation induction, bromodeoxyuridylate incorporation into DNA, and cell viability under various conditions revealed: (1) lethality and mutagenesis can be uncoupled, (2) thymidylate enhances mutagenesis and deoxycytidylate suppresses it, (3) mutation induction is not correlated with the magnitude of bromodeoxyuridylate incorporation into DNA. Therefore, in yeast, the pyrimidine nucleotide pools have a powerful effect on bromodeoxyuridylate mutagenesis. Both bromodeoxyuridylate and iododeoxyuridylate are extensively incorporated into the DNA of tmp1 yeast cells; however, iododeoxyuridylate is nonmutagenic. Replication proceeds at the same rate in the ***presence*** of the natural substrate or either analog. When cells are supplied with thymidylate and bromodeoxyuridylate together, there is no discrimination against bromodeoxyuridylate as a DNA precursor. However, in the ***presence*** of thymidylate and iododeoxyuridylate, there is a 3 to 1 discrimination against iododeoxyuridylate as compared to thymidylate.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L17 ANSWER 108 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1987:62158 CAPLUS <<LOGINID::20100917>>
DN 106:62158
OREF 106:10155a,10158a
TI An efficient chloramphenicol-resistance marker for Saccharomyces cerevisiae and Escherichia coli
AU Hadfield, C.; Cashmore, A. M.; Meacock, P. A.
CS Leicester Biocent., Univ. Leicester, Leicester, LE1 7RH, UK
SO Gene (1986), 45(2), 149-58 CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB Chloramphenicol (Cm) [56-75-7] was demonstrated to be a suitable selective agent for the plasmid-mediated transformation of haploid and polyploid strains of S. cerevisiae. A yeast/E. coli shuttle Cm-resistance (CmR) marker was constructed by inserting the chloramphenicol acetyltransferase [9040-07-7] coding sequence from Tn9, and its assocd. bacterial ribosome-binding site, between a modified yeast ADC1 promoter and CYC1 terminator. When ***present*** on a 2 .mu.m-based replicating plasmid, this marker transformed ***yeast*** as

efficiently as the ***auxotrophic*** markers TRP1 and LEU2. When included in an integrating vector, single-copy transformants were formed as efficiently as with LEU2 and HIS3. Industrial yeast strains were transformed with both the replicating and integrating plasmids. The CmR marker could also efficiently transform E. coli. This versatile and efficient performance is currently unique for a yeast dominant marker.
OSC.G 18 THERE ARE 18 CAPLUS RECORDS THAT CITE THIS RECORD (18 CITINGS)

L17 ANSWER 109 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1987:15541 CAPLUS <<LOGINID::20100917>>
DN 106:15541
OREF 106:2637a,2640a
TI An assessment of the ability of yeast cells to incorporate photolabile fatty acids into their membrane phospholipids in vivo
AU Hibbs, Alan R.; Marzuki, Sangkot
CS Dep. Biochem., Monash Univ., Clayton, 3168, Australia
SO Biochimica et Biophysica Acta, Biomembranes (1986), 862(2), 445-50 CODEN: BBBMBS; ISSN: 0005-2736
DT Journal
LA English
AB The photolabile fatty acids 12-azidooleic, 12-(4-azido-2-nitrophenoxy)oleic, 12-azidolauric and 12-(4-azido-2-nitrophenoxy)lauric acid are readily taken up in vivo by an unsatd. fatty acid ***auxotroph*** of ***Saccharomyces*** ***cerevisiae*** . A low level of the 2 lauric acid derivs. and none of the 2 oleic acid derivs. are incorporated into membrane phospholipids. Under certain conditions of growth in the ***presence*** of 12-(4-azido-2-nitrophenoxy)oleic acid, the nitrophenylazide group is metabolized to a product that lacks the photolabile azido group.

L17 ANSWER 110 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1986:509841 CAPLUS <<LOGINID::20100917>>
DN 105:109841
OREF 105:17691a,17694a
TI DNA sequence polymorphisms in the genus Saccharomyces. IV. Homoeologous chromosomes III of Saccharomyces bayanus, S. carlsbergensis, and S. uvarum
AU Pedersen, Mogens Bohl
CS Dep. Brew. Chem., Carlsberg Res. Lab., Copenhagen Valby, DK-2500, Den.
SO Carlsberg Research Communications (1986), 51(3), 185-202 CODEN: CRCODS; ISSN: 0105-1938
DT Journal
LA English
AB Single chromosome III transfers have been accomplished from the 2 species S. bayanus and S. uvarum into genetically marked S. cerevisiae strains. Incompatibilities between S. bayanus or S. uvarum, and S. cerevisiae strains may account for the very few chromosome addn. lines obtained. The preliminary genetic map for S. bayanus chromosome III is similar to the genetic map for a S. carlsbergensis chromosome III from Danish lager strain BK2208. Recombination is ***absent*** between the transferred chromosomes and the ***auxotrophically*** marked chromosome from S. ***cerevisiae*** in the interval HIS4 to LEU2 but recombination does occur in the interval LEU2 to THR4. The mapped S. bayanus chromosome III carries HIS4 pattern III while the mapped chromosome III from the later strain contains HIS4 pattern II. Transfer of a chromosome III from S. uvarum to S. cerevisiae has been recognized by restriction endonuclease fragment patterns, OFAGE (Orthogonal field alteration gel electrophoresis) chromosome sepns. and mol. hybridization, but a genetic map could not be constructed for an S. uvarum chromosome due to instability of the chromosome addn. lines. The hypothesis is put forward that the S. carlsbergensis type strain and the lager strains are sibling species and species hybrids both produced by hybridization of an S. cerevisiae top fermenting strain and the bottom fermenting strain S. monacensis. The lager strains and the authentic type strain are designated S. carlsbergensis. From the electrophoretic karyotypes of type strains of Saccharomyces and mol. hybridization patterns it is deduced that S. bayanus, S. inusitatus, S. pastorianus and S. uvarum are closely related but distinct from the bottom fermenting strains.
OSC.G 25 THERE ARE 25 CAPLUS RECORDS THAT CITE THIS RECORD (26 CITINGS)

L17 ANSWER 111 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1986:436764 CAPLUS <<LOGINID::20100917>>
DN 105:36764
OREF 105:5993a,5996a
TI Plasmid-transformed URA3 FUR1 double-mutants of S. cerevisiae: an autoselection system applicable to the production of foreign proteins
AU Loison, Gerard; Nguyen-Juilleret, Martine; Alouani, Sami; Marquet, Magda
CS TRANSGENE S. A., Strasbourg, 67000, Fr.
SO Bio/Technology (1986), 4(5), 433-7 CODEN: BTCHDA; ISSN: 0733-222X
DT Journal
LA English
AB Simple ***auxotrophic*** mutants of ***Saccharomyces*** ***cerevisiae*** transformed to prototrophy via plasmid DNA must be grown in media in which cured cells are counter-selected. This restricts the choice of the medium to those whose compn. is compatible with the selection. These media are generally not comparable with the cheap, complex media used by industry for the prodn. of yeast cells. A new selection system that enables the growth of plasmid-transformed yeast cells for the prodn. of foreign proteins in complex media. is reported. The recipient strains are double-mutants (ura3 fur1) whose viability is strictly linked to the ***presence*** of a plasmid encoding a functional orotidine-5'-phosphate decarboxylase [9024-62-8]. These strains can produce high levels of a plasmid-encoded foreign protein (namely human .alpha.1-antitrypsin [9041-92-3]) in various complex media, including those used by industry, for many generations without any detectable loss of the plasmid-linked phenotype.
OSC.G 15 THERE ARE 15 CAPLUS RECORDS THAT CITE THIS RECORD (15 CITINGS)

L17 ANSWER 112 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1986:423060 CAPLUS <<LOGINID::20100917>>
DN 105:23060
OREF 105:3869a,3872a
TI Interspecific protoplast fusion of Saccharomyces cerevisiae and S. mellis. Biochemical and genetic aspects
AU Margalith, P.; Legman, R.
CS Dep. Food Eng. Biotechnol., Technion, Israel Inst. Technol., Haifa, 32000, Israel
SO Eur. Congr. Biotechnol., 3rd (1984), Volume 3, 421-5 Publisher: Verlag Chemie, Weinheim, Fed. Rep. Ger. CODEN: 55BBA6
DT Conference
LA English

AB Protoplast fusion of ***auxotrophic*** mutant of S. ***cerevisiae*** and the osmotolerant S. mellis produced stable hybrids with increased capability of EtOH [64-17-5] fermn. Hybrid strain no. 37 was selected which produced .apprx.13.6% EtOH after 72 h of fermn. (35% glucose [50-99-7]; 30.degree. with gentle shaking) in comparison with 9.0% by the control S. cerevisiae strain. A scheme is ***presented*** for protoplast fusion and isolation of hybrid strains.

L17 ANSWER 113 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1986:221746 CAPLUS <<LOGINID::20100917>>
DN 104:221746
OREF 104:35097a,35100a
TI Release of a lectin from a fatty acid ***auxotroph*** of ***Saccharomyces*** ***cerevisiae*** grown in ***presence*** of oleic acid
AU Basu, Joyoti; Kundu, Manikuntala; Mukherjee, Krishna; Chakrabarti, Parul
CS Dep. Chem., Bose Inst., Calcutta, 700 009, India
SO Biochemical and Biophysical Research Communications (1986), 136(2), 596-602 CODEN: BBRCA9; ISSN: 0006-291X
DT Journal
LA English
AB The unsatd. fatty acid-requiring mutant KD 115 of S. cerevisiae secretes a lectin when grown with oleic acid. This lectin is homogeneous on polyacrylamide gel electrophoresis at pH 8.3, has an approx. mol. wt. of 320,000, pI of 4.2, and contains .apprx.60% sugar. It agglutinates chicken and different mammalian erythrocytes, but lyses rabbit red cells only. It is D-galactose-specific. This is the first report of a hemagglutinin from yeast.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L17 ANSWER 114 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1986:2295 CAPLUS <<LOGINID::20100917>>
DN 104:2295
OREF 104:415a,418a
TI In vitro methylation of undermethylated yeast poly(A)-rich RNA using mRNA (guanine-7-)-methyltransferase purified from wheat germ or yeast
AU Locht, Camille; Delcour, Jean
CS Lab. Genet. Mol., Fac. Univ. Notre-Dame Paix, Namur, Belg.
SO European Journal of Biochemistry (1985), 152(2), 247-51 CODEN: EJBCAI; ISSN: 0014-2956
DT Journal
LA English
AB By crossing 2 strains of Saccharomyces cerevisiae deficient for each of the 2 methionine adenoxyltransferase isoenzymes (EC 2.5.1.6) resp., a strain strictly auxotrophic for S-adenosylmethionine was constructed and used as a source of undermethylated mRNA suitable for in vitro transmethylation studies. RNA was phenol-extd. from yeast cells shifted down to S-adenosylmethionine-free medium for 90 min, and poly(A)-rich RNA was prepd. by oligo(dT)-cellulose chromatog. Upon incubation in vitro in the ***presence*** of Me-labeled S-adenosylmethionine and mRNA (guanine-7-)-methyltransferase purified from wheat germ or yeast, undermethylated poly(A)-rich RNA became significantly labeled as compared to nonstarved cells from the same strain, or from a wild-type control. Cap structures were resolved by paper chromatog. after T2 and P1 RNase digestion, and shown to be a mixt. of m7G5'ppp5'G and m7G5'ppp5'A (m7G = N7-Me guanosine), irresp. of the enzyme source, in agreement with earlier in vivo studies in yeast mRNA capping and methylation.

L17 ANSWER 115 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1985:559023 CAPLUS <<LOGINID::20100917>>
DN 103:159023
OREF 103:25507a,25510a
TI Biosynthesis of tritium-labelled S-adenosyl-L-methionine
AU Myasoedov, N. F.; Kuznetsova, O. B.; Kozik, V. S.
CS Inst. Mol. Genet., Moscow, USSR
SO Bioorganicheskaya Khimiya (1985), 11(7), 944-7 CODEN: BIKHD7; ISSN: 0132-3423
DT Journal
LA Russian
AB Biosynthetic prepn. of S-adenosyl-L-[methyl-3H]methionine [98574-95-9] from L-[methyl-3H]methionine by cultivation of diploid ***Saccharomyces*** ***cerevisiae*** (methionine ***auxotroph***) in a medium with a high concn. of L-methionine is described. The radiochem. purity was >95%. Biol. activity of the prepns. has been shown in transmethylation reactions in the ***presence*** of the yeast homocysteine methyltransferase.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L17 ANSWER 116 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1985:517428 CAPLUS <<LOGINID::20100917>>
DN 103:117428
OREF 103:18697a,18700a
TI Plasmids pEMBLY: new single-stranded shuttle vectors for the recovery and analysis of yeast DNA sequences
AU Baldari, C.; Cesareni, G.
CS Eur. Mol. Biol. Lab., Heidelberg, D-6900, Fed. Rep. Ger.
SO Gene (1985), 35(1-2), 27-32 CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB The construction and properties of pEMBLY plasmids is described. The plasmids belong to a new family of yeast shuttle vectors which are derived from plasmid vector pEMBL9 and offer the following improvements: relatively small size, large no. of cloning sites, the screening for insert-contg. plasmids on indicator plates, different combinations of genes which complement ***auxotrophic*** deficiencies and sequences that support DNA replication in ***Saccharomyces*** ***cerevisiae*** , and the ability to isolate the plasmid DNA in single-stranded (ss) form. The yeast S. cerevisiae can be efficiently transformed by these plasmids in both the ss and double-stranded forms. Finally, the ***presence*** of the phage f1 intergenic region allows the cloned sequences to be obtained in the ss form upon infection with the wild-type ss phage.
OSC.G 18 THERE ARE 18 CAPLUS RECORDS THAT CITE THIS RECORD (18 CITINGS)

L17 ANSWER 117 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1985:468119 CAPLUS <<LOGINID::20100917>>
DN 103:68119
OREF 103:10909a,10912a
TI Genetic and molecular characterization of a distiller's yeast
AU Keiding, Anne Kristine
CS Dan. Distill. Ltd., Copenhagen, DK-2300, Den.
SO Carlsberg Research Communications (1985), 50(2), 95-125 CODEN: CRCODS; ISSN: 0105-1938

DT Journal
LA English
AB Auxotrophic mutants were induced by UV-irradn. and EMS treatment in meiotic segregants of a distiller's prodn. strain of yeast. In complementation ***tests*** some of the mutants were allelic to ade1, ade3, Lys2, met13, trp1., ura1, and ura4 of std. strains of S. cerevisiae. Crosses were made between 2 spore-derived clones of the distller's strain and haploid S. cerevisiae strains carrying several autotrophic markers. Tetrad anal. of the mating products revealed that the spore-derived clones were disomic for 6 and 7 chromosomes, resp. Chromosomes III from the distiller's prodn. strain were compared to their counterparts in std. strains of S. cerevisiae at several loci. Cloned DNA from HIS4, LEU2, and MAT loci from the std. strain were used as hybridization probes to ***test*** the nucleotide sequence homol. at the loci and the silent mating type genes HML and HMR. Restriction site polymorphisms were not detected inside the loci, but in regions adjacent to them. These could be exploited in combination with tetrad anal. to identify 4 different chromosomes III in the distiller's strain. Of the 4 chromosomes, 3 were lacking HML and 1 was lacking HMR. Thus, all loci ***tested*** are organized in the same order as in the genetically analyzed std. strains.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L17 ANSWER 118 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1985:126632 CAPLUS <<LOGINID::20100917>>
DN 102:126632
OREF 102:19801a,19804a
TI Production of catechol 2,3-oxygenase by means of yeasts, plasmid for the implementation thereof and application
IN Aigle, Michel; Lemoine, Yves; Loison, Gerard; Lecocq, Jean Pierre
PA Transgene S. A., Fr.
SO PCT Int. Appl., 52 pp. CODEN: PIXXD2
DT Patent
LA French
FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE ---------- ---- -------- ---------- --------
PI WO 8404539 A1 19841122 WO 1984-FR133 19840517 W: DK, JP, US RW: AT, BE, CH, DE, FR, GB, LU, NL, SE FR 2546179 A1 19841123 FR 1983-8292 19830519 FR 2546179 B1 19851220 FR 2561662 A2 19850927 FR 1984-4453 19840322 FR 2561662 B2 19860822 EP 143821 A1 19850612 EP 1984-902017 19840517 R: AT, BE, CH, DE, FR, GB, LI, LU, NL, SE JP 60501289 T 19850815 JP 1984-501927 19840517 DK 8500273 A 19850118 DK 1985-273 19850118
PRAI FR 1983-8292 A 19830519 FR 1984-4453 A 19840322 WO 1984-FR133 W 19840517
AB The enzyme catechol 2,3-oxygenase [9029-46-3] is responsible for the conversion of catechol [120-80-9], a colorless compd. to the muconic acid 2-hydroxysemialdehyde [3270-98-2], a yellow compd. Shuttle vectors are constructed, for cloning in yeast or Escherichia coli, that contain the Pseudomonas plasmid TOL gene xylE for catechol 2,3-oxygenase, and the color change, colorless to yellow, is used an indicator. Thus, plasmid pTG821, which contained the promoter, coding, and termination region of the yeast gene URA3 and gene xylE, (the gene xylE expression block) was constructed. The expression block was cloned into the HindIII site of plasmid pJDB207 to yield plasmid pJDB207-xylE. Plasmid pJDB207-xylE contained the xylE expression block, the yeast 2 .mu.m plasmid and E. coli replication origins, a yeast selective marker for leucine formation, and an E. coli selective marker for ampicillin [69-53-4] resistance. Plasmid pJDB207-xylE was used to transform protoplasts of a strain of ***yeast*** ***auxotrophic*** for leucine. Clones were selected on the basis of leucine prototrophy. The ***presence*** of catechol 2,3-oxygenase was examd. by spraying the colonies with 0.5 M catechol. Colonies that expressed the enzyme turned a deep yellow. The gene xylE expression block was also inserted directly into the yeast chromosome V. However, only very low quantities of catechol 2,3-oxygenase were produced. Plasmid pTG861 was constructed to clone gene xylE in industrial yeasts, i.e. bakers' or brewers' yeast. The plasmid contained the E. coli origin of replication, the E. coli gene for ampicillin resistance, the yeast 2 .mu. plasmid origin of replication, the yeast phosphoglycerate kinase [9001-83-6] promoter and termination regions, the selective marker for antibiotic G418 [49863-47-0]-resistance from plasmid pNeo, and the xylE expression block.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)
RE.CNT 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 119 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1984:487134 CAPLUS <<LOGINID::20100917>>
DN 101:87134
OREF 101:13329a,13332a
TI Protoplast fusion between a petite strain of Candida utilis and Saccharomyces cerevisiae respiratory-competent cells
AU De Richard, Mirta S.; De van Broock, Maria R.
CS Pilot Plant Ind. Microbiol. Processes, PROIMI, Tucuman, 4000, Argent.
SO Current Microbiology (1984), 10(3), 117-20 CODEN: CUMIDD; ISSN: 0343-8651
DT Journal
LA English
AB Prototrophic RD mutant cells of C. utilis NRRL-Y-1084 and ***auxotrophic*** mutant respiratory-competent cells of S. ***cerevisiae*** 4003-5B a his4 leu2 canS meth2 trp5 ade1 ura3 gal were turned into protoplasts to be further fused with the aid of polyethylene glycol (PEG) and Ca2+. Minimal medium contg. glycerol as the C source was employed for fusion product selection. The respiratory-competent fusion products, mainly oval cells, resembled C. utilis and had the fermentative abilities of this strain (glucose, sucrose, raffinose). Five fusion products were analyzed as to their ability to metabolize glucose, xylose, cellobiose, trehalose, glycerol, succinic acid, citric acid, salicin, and maltose. Fusion products partially restored the respiratory-competent C. utilis capacity to grow by use of these C compds., and none of the S. cerevisiae fermenting abilities were found. The results suggest either a partial recombination between parental mitochondria or some occurring phenomenon affecting the cell membrane function after somatic fusion without concomitant nuclear fusion.

L17 ANSWER 120 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1984:435797 CAPLUS <<LOGINID::20100917>>
DN 101:35797
OREF 101:5561a,5564a
TI Susceptibility of Saccharomyces spp. and Schwanniomyces spp. to the aminoglycoside antibiotic G418

AU Panchal, Chandra J.; Whitney, Gordon K.; Stewart, Graham G.
CS Prod. Res. Dep., Labatt Brewing Co. Ltd., London, ON, N6A 4M3, Can.
SO Applied and Environmental Microbiology (1984), 47(5), 1164-6 CODEN: AEMIDF; ISSN: 0099-2240
DT Journal
LA English
AB Industrially useful polyploid ***yeasts*** , such as the brewers' ***yeast*** , do not possess any ***auxotrophic*** genetic markers and hence are not easily amenable to plasmid-mediated DNA transformations. In an attempt to obtain genetic markers, a no. of useful Saccharomyces strains and some amylolytic Schwanniomyces strains were ***tested*** for their susceptibility to Geneticin G418. All of the Saccharomyces strains, including the brewers' strains, were susceptible to G418 in the concn. range of 150-1402 .mu.g/mL. Of the Schwanniomyces species investigated, only S. castellii was resistant to G418 at <1 mg/mL. Resistance was exhibited both in liq. media and on glycerol-peptone-yeast ext. agar plates. This finding is interesting in view of the possibility of using this strains as a DNA donor for transformations aimed at introducing the amylolytic capability into brewers' yeasts.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L17 ANSWER 121 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1984:171335 CAPLUS <<LOGINID::20100917>>
DN 100:171335
OREF 100:26005a,26008a
TI Regulation in yeasts via steroids
AU Kumari, S. Nanda; Lala, Anil K.
CS Dep. Chem., IIT, Bombay, 400 076, India
SO Proc. Symp. Cell. Control Mech. (1983), Meeting Date 1982, 254-8 Publisher: Dep. At. Energy, Bombay, India. CODEN: 51GBA3
DT Conference
LA English
AB The impact of sterol structure on the growth of a sterol-requiring double mutant (GL-7) of Saccharomyces cerevisiae was examd. with a series of cholesterol analogs. No growth of the yeast mutant occurred with dehydroepiandrosterone, 5.alpha.-cholestane, androst-5en-3.beta.-ol, epicholesterol, and 3.beta.-hydroxy-3.alpha.-methyl-5.alpha.-cholestane. Cholestan-3.beta.-ol showed only 64% of the effectiveness of cholesterol in supporting growth, which suggested that the ***presence*** or ***absence*** of a 5,6-double bond makes a difference. This suggestion was supported by results with cholestan-3.alpha.-ol, which was nearly as effective as cholestan-3.beta.-ol. The compd. 3.alpha.-hydroxy-3.beta.-methyl-5.alpha.-cholestane supported growth as well as did 5.alpha.-cholestan-3.alpha.-ol. Thus, minor structural variations of ring A of cholesterol were responsible for alteration in the growth pattern of mutant GL-7, probably by their effects on membrane functions.

L17 ANSWER 122 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1984:171309 CAPLUS <<LOGINID::20100917>>
DN 100:171309
OREF 100:26001a,26004a
TI Isolation of uracil ***auxotrophic*** mutants of ***Saccharomyces*** ***cerevisiae*** unable to reduce 2,3,5-triphenyltetrazolium chloride
AU Ouchi, Kozo; Shimoi, Hitoshi; Shimoda, Masahiko; Akiyama, Hiroichi; Nishiya, Takamichi
CS Natl. Res. Inst. Brew., Tokyo, 114, Japan
SO Agricultural and Biological Chemistry (1984), 48(2), 473-6 CODEN: ABCHA6; ISSN: 0002-1369
DT Journal
LA English
AB A new type of mutant unable to reduce 2,3,5-triphenyltetrazolium chloride (TTC) was isolated from mutagenized cells of S. cerevisiae. These TTC- mutants were respiration-competent, although most TTC- mutants reported so far are respiration-deficient. The isolated mutants were also auxotrophic for uracil, and genetic anal. indicated that a recessive mutation took place on a single gene tightly linked to the ura2 gene or in the ura2 gene in all these mutants. Moreover, authentic ura mutants (ura1 to ura5) also exhibited the TTC- phenotype, whereas other auxotrophic mutants ***tested*** were of the TTC+ phenotype. Apparently, yeast cells have a TTC redn. system related to uracil metab. besides that related to respiratory potential.

L17 ANSWER 123 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1984:169324 CAPLUS <<LOGINID::20100917>>
DN 100:169324
OREF 100:25669a,25672a
TI Yeast LEU1. Repression of mRNA levels by leucine and relationship of 5'-noncoding region to that of LEU2
AU Hsu, Yun Pung; Schimmel, Paul
CS Dep. Biol., Massachusetts Inst. Technol., Cambridge, MA, 02139, USA
SO Journal of Biological Chemistry (1984), 259(6), 3714-19 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB The yeast gene LEU1 encodes the 2nd enzyme in leucine [61-90-5] biosynthesis. A 3.5-kilobase (kb) ***yeast*** genomic DNA fragment which complements a leu1 ***auxotroph*** was isolated by ***yeast*** transformation. After recloning into an integrating vector, a subfragment (of the 3.5-kb fragment) directs a URA3 marker to integrate at the LEU1 locus. About 1.9 kb was sequenced from the 5'-end of the 3.5-kb insert, and a long open reading frame and potential ATG start codon were located. S1 nuclease mapping showed a major start for LEU1 transcripts at 79 nucleotides upstream of the ATG codon. Northern blots with a LEU1-specific probe showed the size of the LEU1 transcript (.apprx.2.9 kb) is consistent with the size of the enzyme, and steady state levels of the transcript are sharply reduced in cells grown in the ***presence*** of an elevated leucine concn. The latter observation correlates with the repression by leucine of LEU1 gene product levels. Other work showed that the level of the LEU2 gene product is also repressed by leucine. Sequence comparisons between LEU1 and LEU2 show that the LEU2 5'-sequences which are cognate to leucine are not found in LEU1. Three blocks of nucleotide sequence homol. between LEU1 and LEU2 occur in the 330 nucleotides upstream of the resp. start codons.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)

L17 ANSWER 124 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1984:153696 CAPLUS <<LOGINID::20100917>>
DN 100:153696
OREF 100:23373a,23376a

TI New markers in the Peterhoff genetic stock yeasts
AU Sambuk, E. V.; Maarich, M. A.; Sharypova, L. A.; Kozhin, S. A.
CS USSR
SO Vestnik Leningradskogo Universiteta, Seriya 3: Biologiya (1984), (1), 90-5 CODEN: VLUBB6; ISSN: 0301-6870
DT Journal
LA Russian
AB Newly isolated ***auxotrophic*** mutations of the Peterhoff ***yeast*** breeding stocks were found to be allelic to his1, ilv1, lys1, arg4, leu1, trp5, and asp5 genes. Linkage studies with these auxotrophic mutations were undertaken to support the results of complementation ***tests*** . Recombinational anal. revealed a centromere linkage of genes allelic to lys1, arg4, leu1, trp5, and asp5. Genes allelic to his1 and ilv1 were linked to each other. These data are consistent with the map location of the resp. genes. Three new linkage groups of Peterhoff yeast breeding stocks were identified during this study.

L17 ANSWER 125 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1984:151877 CAPLUS <<LOGINID::20100917>>
DN 100:151877
OREF 100:23053a,23056a
TI Direct selection of Saccharomyces cerevisiae resistant to the antibiotic G418 following transformation with a DNA vector carrying the kanamycin-resistance gene of Tn903
AU Webster, Thomas D.; Dickson, Robert C.
CS Coll. Med., Univ. Kentucky, Lexington, KY, 40536-00840, USA
SO Gene (1983), 26(2-3), 243-52 CODEN: GENED6; ISSN: 0378-1119
DT Journal
LA English
AB A new procedure was developed for selecting ***yeast*** transformants without the need for complementing ***auxotrophic*** markers. The procedure is based on resistance to antibiotic G418 [49863-47-0] imparted to transformants by recombinant DNA vectors. Several Escherichia coli-yeast shuttle vectors contg. the kanamycin [8063-07-8] (G418)-resistance gene of Tn903, plus several yeast genes making dual selections possible were constructed. The efficiency for selecting G418-resistant transformants was dependent upon several factors including the compn. of the growth medium and the time at which G418 selective pressure was administered. Media which contained levels of salts found in yeast N base rendered cells partially to completely resistant to G418 and could not be used for selecting G418-resistant transformants. On the other hand, untransformed cells remained sensitive to G418 when grown on YEPD medium thus allowing selection of G418-resistant transformants. A lag phase of 12-18 h, following growth at 30.degree., was required prior to administration of G418 to achieve max. transformation frequency. Transformation frequencies ranged 100-700/.mu.g of DNA and varied with the vector and strain used. The kanamycin gene imparted resistance to G418 in either the episomally or chromosomally integrated state. The gene was highly stable in the integrated state, even without selective pressure. The utility of the procedure was demonstrated by selecting transformants of 4 different strains of S. cerevisiae and by cloning autonomous replication sequences (ARS) from the yeast Kluyveromyces lactis. This or related procedures could be used to develop transformation systems for many eukaryotic and prokaryotic cells for which no transformation procedure is available.
OSC.G 17 THERE ARE 17 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)

L17 ANSWER 126 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1984:32011 CAPLUS <<LOGINID::20100917>>
DN 100:32011
OREF 100:4935a,4938a
TI Growth of a sterol ***auxotroph*** derived from ***Saccharomyces*** ***cerevisiae*** on chemically synthesized derivatives of cholesterol possessing side-chain modifications
AU Rodriguez, R. J.; Arunachalam, T. A.; Parks, L. W.; Caspi, E.
CS Dep. Microbiol., Oregon State Univ., Corvallis, OR, 97331-3804, USA
SO Lipids (1983), 18(11), 772-5 CODEN: LPDSAP; ISSN: 0024-4201
DT Journal
LA English
AB A no. of cholesterol derivs. were analyzed for their ability to satisfy bulk membrane and high-specificity sparking requirements of a ***yeast*** sterol ***auxotroph*** (RD5-R). Substitution of H by Br or I at C-26 or substitution of C26-Me by Br enabled the resulting sterol to satisfy bulk or sparking functions. The ***presence*** of a side-chain hydroxyl or keto group at C-25 on a 26-norcholesterol completely abolished the ability of cholesterol to satisfy either sterol requirement. Growth studies revealed that, while the oxygenated cholesterol derivs. were not growth-supportive of RD5-R, they were not growth-inhibitory.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L17 ANSWER 127 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1983:611084 CAPLUS <<LOGINID::20100917>>
DN 99:211084
OREF 99:32469a,32472a
TI Reduction of higher alcohols by fermentation with a leucine-***auxotrophic*** mutant of wine ***yeast***
AU Rous, C. V.; Snow, R.; Kunkee, R. E.
CS Dep. Genet., Univ. California, Davis, CA, 95616, USA
SO Journal of the Institute of Brewing (1983), 89(4), 274-8 CODEN: JINBAL; ISSN: 0368-2587
DT Journal
LA English
AB Several auxotrophic mutants requiring branched-chain amino acids (valine, leucine, or isoleucine) were isolated in a strain of Montrachet wine yeast. They were ***tested*** for their ability to produce less higher alcs. (fusel oil, isobutyl [78-83-1], isoamyl [123-51-3], and active amyl [137-32-6] alcs.) in grape juice fermns. One strain which required leucine was esp. good in this respect. This mutation is recessive and is the result of a deficiency for the enzyme .alpha.-isopropylamate dehydratase. In trial fermns. with this mutant, the resulting wines contained up to 20% less total fusel oil and 50% less isoamyl alc. than the parent Montrachet strain. An experienced taste panel did not discern any gross degrdn. of taste quality in wine made with the mutant strain compared to that made with the parent strain. The mutant strain could be of com. importance in prepn. of distg. material for alc. beverages since the reduced fusel oil content would not require any special distn. procedures which are normally used to avoid the unpleasant flavor assocd. with concd. higher alcs. Redn. of the isoamyl alc. content is particularly significant since this fusel oil component is usually ***present*** in the highest amt.

OSC.G 10 THERE ARE 10 CAPLUS RECORDS THAT CITE THIS RECORD (10 CITINGS)

L17 ANSWER 128 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1983:466494 CAPLUS <<LOGINID::20100917>>
DN 99:66494
OREF 99:10285a,10288a
TI Partial purification and characterization of mRNA (guanine-7-)methyltransferase from the yeast Saccharomyces cerevisiae
AU Locht, Camille; Beaudart, Jean Luc; Delcour, Jean
CS Unite Genet. Mol. Eucaryotes, Univ. Cathol. Louvain, Louvain-la-Neuve, Belg.
SO European Journal of Biochemistry (1983), 134(1), 117-21 CODEN: EJBCAI; ISSN: 0014-2956
DT Journal
LA English
AB As a tool for the study of the capping-methylation process of yeast mRNA, a procedure was developed for the purifn. of mRNA guanine 7-methyltransferase (I) using the com. cap analog guanosine(5')triphospho(5')guanosine as a substrate and radioactive S-adenosylmethionine (II) as the Me group donor. The osmotic-sensitive yeast strain VY1160 was used as the enzyme source. Little I activity was detectable in a crude lysate obtained after osmotic shock. This was due to the ***presence*** of a low-mol.-wt. inhibitor which could easily be eliminated by Sephadex G-25 gel filtration. The 10,000 g supernatant from the crude lysate was submitted to DEAE-cellulose and DNA-agarose chromatog. The resulting prepn. was enriched .apprx.450-fold in specific activity. Under std. assay conditions, the incorporation rate remained const. for .gtoreq.6 h at 30.degree.. Transmethylation was not stimulated by KCl or NaCl. Divalent cations were strong inhibitors. Partially purified I was able to methylate undermethylated poly(A)-rich mRNA isolated from a II ***auxotrophic*** ***yeast*** strain briefly exposed to II-free medium.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L17 ANSWER 129 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1983:419443 CAPLUS <<LOGINID::20100917>>
DN 99:19443
OREF 99:3105a,3108a
TI Dependence on cyclic AMP of glucose-induced inactivation of yeast gluconeogenetic enzymes
AU Tortora, Paolo; Burlini, Nedda; Leoni, Flavio; Guerritore, Andrea
CS Dip. Fisiol. Biochim. Gen., Univ. Milano, Milan, I-20133, Italy
SO FEBS Letters (1983), 155(1), 39-42 CODEN: FEBLAL; ISSN: 0014-5793
DT Journal
LA English
AB The extent of catabolite inactivation of fructose, 1,6-diphosphatase, malate dehydrogenase, and phosphoenolpyruvate carboxykinase and the glucose-induced peak of intracellular cAMP concn. were measured in 2 haploid mutants of ***Saccharomyces*** ***cerevisiae*** , AM3-4B, which is ***auxotrophic*** for adenine and able to incorporate AMP and cAMP from the medium, and AM7-11D, which was isolated from the previous one and which is adenylate cyclase-deficient. The ***absence*** of the inactivating effect of glucose in the strain defective for cAMP synthesis indicates the involvement of cAMP in the inactivation process.

L17 ANSWER 130 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1983:175706 CAPLUS <<LOGINID::20100917>>
DN 98:175706
OREF 98:26645a,26648a
TI Ploidy reduction using p-fluorophenylalanine of fusion products of Saccharomyces cerevisiae
AU De van Broock, Maria R.; Sierra, Mirta; De Figueroa, Lucia C.
CS Planta Piloto Procesos Ind. Microbiol. Avda. Belgrano, PROIMI, Tucuman, 4000, Argent.
SO Current Microbiology (1983), 8(1), 13-16 CODEN: CUMIDD; ISSN: 0343-8651
DT Journal
LA English
AB Fusion of yeast protoplasts was induced in the ***presence*** of polyethylene glycol and Ca2+. Two ***auxotrophic*** complementing S. ***cerevisiae*** mutant strains were used in fusion expts. One diploid and several polyploid fusion products were selected by complementation in minimal medium. The assessment of ploidy was based on the DNA content of the parental cells and fusion products assayed by the diphenylamine method. By treating the fusion product cells with p-fluorophenylalanine, parental his and leu markers could not be recovered. Instead, a strong redn. of polyploid fusion product cell DNA content was evident. The anal. of meiotic products after hybridizing 1 fusion product with a prototrophic S. cerevisiae std. strain led to the recovery of the his parental marker. Preliminary evidence that p-fluorophenylalanine can be used as a diploidizing agent towards polyploid strains of S. cerevisiae is reported.

L17 ANSWER 131 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1983:138339 CAPLUS <<LOGINID::20100917>>
DN 98:138339
OREF 98:20971a,20974a
TI Nonsense suppression in Schizosaccharomyces pombe: the S. pombe Sup3-e tRNAUGASer gene is active in S. cerevisiae
AU Hottinger, Herbert; Pearson, David; Yamao, Fumiaki; Gamulin, Vera; Cooley, Lynn; Cooper, Terrance; Soll, Dieter
CS Mol. Biophys. Biochem., Yale Univ., New Haven, CT, 06511, USA
SO Molecular and General Genetics (1982), 188(2), 219-24 CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB The gene encoding the efficient UGA suppressor sup3-e of S. pombe was isolated by in-vivo transformation of Saccharomyces cerevisiae UGA mutants with S. pombe sup3-e DNA. DNA from a clone bank of EcoRI fragments from a S. pombe sup3-e strain in the hybrid ***yeast*** vector YRp17 was used to transform the S. ***cerevisiae*** multiple ***auxotroph*** his4-260 leu2-2 trp1-1 to prototrophy. Transformants were isolated at a low frequency; they lost the ability to grow in minimal medium after passaging in nonselective media. This suggested the ***presence*** of the suppressor gene on the nonintegrative plasmid. Plasmid DNA, isolated from the transformed S. cerevisiae cells and subsequently amplified in Escherichia coli, transformed S. cerevisiae his4-260 leu2-2 trp1-1 to prototrophy. In this way, a 2.4-kilobase S. pombe DNA fragment carrying the sup3-e gene was isolated. Sequence anal. revealed the ***presence*** of 2 tRNA coding regions sepd. by a spacer of only 7 nucleotides. The sup3-e tRNAUGASer gene is followed by a sequence coding for the initiator tRNAMet. The transformation results demonstrate that the cloned S. pombe UGA suppressor is active in S. cerevisiae UGA mutant strains.

OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)

L17 ANSWER 132 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1983:102896 CAPLUS <<LOGINID::20100917>>
DN 98:102896
OREF 98:15625a,15628a
TI Complete nuclear magnetic resonance signal assignments and initial structural studies of [13C]methyl-enriched yeast transfer ribonucleic acid
AU Agris, Paul F.; Kovacs, Shirley A. H.; Smith, Christine; Kopper, Randall A.; Schmidt, Paul G.
CS Div. Biol. Sci., Univ. Columbia, Columbia, MO, 65211, USA
SO Biochemistry (1983), 22(6), 1402-8 CODEN: BICHAW; ISSN: 0006-2960
DT Journal
LA English
AB 13C enrichment of Me groups of yeast tRNA in vivo has produced probes that do not perturb native tRNA structure, are located at 19 distinct sequence positions, and are sensitive to structural perturbations of the RNA. Exclusive 13C enrichment of Me groups was accomplished by design of a medium for optimal growth of cultures and maximal post-transcriptional incorporation of [13C]Me groups into nucleic acids of a methionine ***auxotroph*** of ***Saccharomyces*** ***cerevisiae*** . 13C-enriched tRNA isolated from these cultures and [3H]Me-labeled tRNA isolated from analogous cultures grown with [3H]methylmethionine were fully methylated as detd. by high-performance liq. chromatog. anal. of nucleosides. Ninety-two percent of the radiochem. label was found assocd. with methylated nucleosides. 13C NMR spectra of 13C-enriched tRNA exhibited prominent high-field, Me signals between 11 and 60 ppm. Integration of signal area relative to that of the natural abundance (1.1%) ribose C atoms indicated a 50-60 atom% [13C]Me enrichment. Signal assignments were made for the Me C atoms of ribothymidine, 5-methylcytidine, N2-methylguanosine, 3-methylcytidine, 1-methylguanosine, 1-methyladenosine, 7-methylguanosine (m7G), N2,N2-dimethylguanosine, 5-(methoxycarbonylmethyl)uridine, and the 2'-O-Me derivs. of cytidine, guanosine, and uridine. These nucleosides are known to be located at 19 sequence positions in loops and stem regions of the cloverleaf structure and the 1st position of the anticodon. Addn. of Mg2+ caused significant line broadening of the yeast tRNA Me signals, in comparison to other yeast tRNA signals and to all signals of [13C]Me-enriched Escherichia coli tRNA. One possible explanation for the difference between the tRNAs of these organisms is an inherent greater variety of tertiary structures probed by the Me groups of yeast tRNA vs. that of E. coli. Me signal chem. shifts moved, on the av., 0.5 ppm upfield with addn. of Mg2+ and downfield with heat denaturation of the tRNA. The exception to this was the resonance for m7G, which displayed the opposite behavior. Me resonances of ribothymidine and 2'-O-Me nucleosides exhibited low-temp. (20-40.degree.) downfield shifts in the ***absence*** of Mg2+ corresponding to temps. expected to break tertiary interactions between the T.psi.CG loop and the dihydrouridine loop in which these Me groups reside. Me signals for N2-methylguanosine and N2,N2-dimethylguanosine exhibited significant downfield shifts at temps. of >40.degree. corresponding to temps. at which secondary structure is expected to dissolve. Relaxation and nuclear Overhauser effect measurements yielded unique solns. for the overall rotational correlation time (10-20 ns) and internal motion correlation times (0.6-2 ps) for the different Me groups. Thus, 13C-enriched Me groups of yeast tRNA will serve as probes of local dynamics at unambiguously assigned locations throughout the mol.

L17 ANSWER 133 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1983:86015 CAPLUS <<LOGINID::20100917>>
DN 98:86015
OREF 98:13089a,13092a
TI Sterol synergism in yeast
AU Ramgopal, Malathi; Bloch, Konrad
CS Dep. Chem., Harvard Univ., Cambridge, MA, 02138, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1983), 80(3), 712-15 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB Sterol synergism, defined as a greater than additive growth response to pairs of sterols, is demonstrated in the ***yeast*** mutant GL7, which is ***auxotrophic*** for sterol and unsatd. fatty acid. Mutant cells growing poorly when provided with cholesterol and oleic acid respond to ergosterol supplements (ergosterol-to-cholesterol ratio, 1:3) by a pronounced increase in growth rates and cell yields. Stigmasterol also elicits a significant synergistic effect; and 7-dehydrocholesterol, a smaller one. Evidence for a metabolic role of ergosterol in yeast membranes is ***presented*** . Cells raised on a 1:3 mixt. of ergosterol to cholesterol up to mid-logarithmic phase subsequently incorporate [1-14C]oleic acid at significantly faster rates into phospholipids than do cells grown on cholesterol alone.
OSC.G 23 THERE ARE 23 CAPLUS RECORDS THAT CITE THIS RECORD (25 CITINGS)

L17 ANSWER 134 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1982:469069 CAPLUS <<LOGINID::20100917>>
DN 97:69069
OREF 97:11503a,11506a
TI Nitrogen catabolite repression in a glutamate ***auxotroph*** of ***Saccharomyces*** ***cerevisiae***
AU Kang, Ling; Keeler, Marilyn L.; Dunlop, Patricia C.; Roon, Robert J.
CS Dep. Biochem., Univ. Minnesota, Minneapolis, MN, 55455, USA
SO Journal of Bacteriology (1982), 151(1), 29-35 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB The biosynthesis of asparaginase II in S. cerevisiae is subject to N catabolite repression. The physiol. effects of glutamate auxotrophy on cellular metab. and on the N catabolite repression of asparaginase II were examd. Glutamate auxotrophic cells, incubated without a glutamate supplement, had a diminished internal pool of .alpha.-ketoglutarate and a concomitant inability to equilibrate NH4+ with .alpha.-amino N. In the glutamate auxotroph, asparaginase II biosynthesis exhibited a decreased sensitivity to N catabolite repression by NH4+, but normal sensitivity to N catabolite repression by all amino acids ***tested*** .
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L17 ANSWER 135 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1982:420462 CAPLUS <<LOGINID::20100917>>
DN 97:20462

OREF 97:3569a,3572a
TI A requirement for ergosterol to permit growth of ***yeast*** sterol ***auxotrophs*** on cholestanol
AU Rodriguez, Russell J.; Taylor, Fred R.; Parks, Leo W.
CS Dep. Microbiol., Oregon State Univ., Corvallis, OR, 97331-3804, USA
SO Biochemical and Biophysical Research Communications (1982), 106(2), 435-41 CODEN: BBRCA9; ISSN: 0006-291X
DT Journal
LA English
AB The ability of cholestanol to support growth of 2 independently derived sterol auxotrophs, FY3 and GL7, was examd. Growth on this stanol was precluded unless minute quantities of sterol were also available. Contaminating sterol in most cholestanol prepns. or excess sterol in the inoculum used in growth studies could provide the required sterol in quantities capable of sustaining growth through an entire culture cycle. Evidence is ***presented*** for multiple functions of sterols in Saccharomyces cerevisiae.
OSC.G 22 THERE ARE 22 CAPLUS RECORDS THAT CITE THIS RECORD (22 CITINGS)

L17 ANSWER 136 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1982:402765 CAPLUS <<LOGINID::20100917>>
DN 97:2765
OREF 97:567a,570a
TI Specific transfer of the hydrogen (HSi) atom of succinate to the 5-deazaflavin analog of succinate dehydrogenase
AU Strobel, Hans Joachim; Retey, Janos
CS Inst. Org. Chem., Univ. Karlsruhe, Karlsruhe, D-7500/1, Fed. Rep. Ger.
SO Angewandte Chemie (1982), 94(5), 396-7 CODEN: ANCEAD; ISSN: 0044-8249
DT Journal
LA German
AB A 5-deazaflavin (I)-contg. succinate dehydrogenase (II) was constructed by incubation of mitochondria of a ***yeast*** flavin ***auxotroph*** with I under aerobic conditions. This modified II had a similar electrophoretic mobility to that of natural II, but the fluorescence emission spectrum was altered. Also, the modified II did not catalyze oxidn. of succinate with O and artificial electron acceptors such as K3Fe(CN)6. The stereospecificity of the natural II from yeast was nearly the same as that of the porcine heart mitochondrial II, as shown by the 3H kinetic isotope effect of HRe and HSi splitting on succinate and 3H exchange. For the modified II of yeast, 3H was transferred only from the S-[2-3H]-succinate to II and not from R-[2-3H]-succinate. The 3H/14C ratio of the products from reaction of modified II with [2-3H,U-14C]-succinate decreased to half the value for the original substrate (in the ***presence*** of fumarase), independently of the chirality of the succinate (R vs. S). Thus, the HSi in succinate is the one transferred to N-5 of riboflavin and the corresponding C atom of I. The stereochem. of this transfer is shown graphically.

L17 ANSWER 137 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1982:136981 CAPLUS <<LOGINID::20100917>>
DN 96:136981
OREF 96:22417a,22420a
TI Expression of the Herpes simplex virus thymidine kinase gene in Saccharomyces cerevisiae
AU McNeil, James B.; Friesen, James D.
CS Dep. Biol., York Univ., Toronto, ON, M3J 1P3, Can.
SO Molecular and General Genetics (1981), 184(3), 386-93 CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB Yeast plasmids were constructed that carry the herpes simplex virus type 1 (HSV-1) thymidine kinase (TK) [9002-06-6] gene which is functionally expressed in S. cerevisiae. The expression of the TK gene appears to be due to transcriptional read-through from a yeast promoter that lies on the 3' side of the HIS3 gene. The TK+ yeast possesses in vitro thymidine kinase activity which is ***absent*** in the original yeast strain. ***Yeast*** strains ***auxotrophic*** for thymidine monophosphate (dTMP) (tmp1) can grow on thymidine [50-89-5]-contg. medium after transformation with these plasmids. Tmp+, TK+ S. cerevisiae whose de novo synthesis of dTMP is inhibited with amethopterin plus sulfanilamide is also capable of growth in thymidine. S. cerevisiae Transformed with such plasmids is capable of incorporating thymidine and bromodeoxyuridine [59-14-3] into DNA.
OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)

L17 ANSWER 138 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1982:82509 CAPLUS <<LOGINID::20100917>>
DN 96:82509
OREF 96:13513a,13516a
TI Inositol mutants of Saccharomyces cerevisiae: mapping the ino1 locus and characterizing alleles of the ino1, ino2 and ino4 loci
AU Donahue, Thomas F.; Henry, Susan A.
CS Dep. Genet. Mol. Biol., Albert Einstein Coll. Med., New York, NY, USA
SO Genetics (1981), 98(3), 491-503 CODEN: GENTAE; ISSN: 0016-6731
DT Journal
LA English
AB An extensive genetic anal. of inositol ***auxotrophic*** mutants of ***yeast*** is reported. The anal. includes newly isolated mutants, as well as those previously reported. Approx. 70% of all the inositol auxotrophs isolated are alleles of the ino1 locus, the structural gene for inositol-1-phosphate synthase, the major enzyme involved in inositol biosynthesis. Alleles of 2 other loci (ino2 and ino4) comprise 9% of the total mutants, with the remainder representing unique loci or complementation groups. The ino1 locus was mapped by trisomic anal. with an n + 1 disomic strain constructed with complementing alleles at this locus. The ino1 locus is located between ura2 (11.1 centimorgans) and cdc6 (21.8 centimorgans) on chromosome X. An extended map of chromosome X of yeast is ***presented*** . Unlike most yeast loci, but like the his1 locus, the ino1 locus lacks allelic representatives that are suppressible by known suppressors. This finding suggests that premature termination of translation of the ino1 gene product may be incompatible with cell viability.
OSC.G 17 THERE ARE 17 CAPLUS RECORDS THAT CITE THIS RECORD (17 CITINGS)

L17 ANSWER 139 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1982:16996 CAPLUS <<LOGINID::20100917>>
DN 96:16996
OREF 96:2831a,2834a
TI Proteolytically induced changes in the molecular form of the carbamyl phosphate synthetase-uracil-aspartate

transcarbamylase complex coded for by the URA2 locus in Saccharomyces cerevisiae
AU Denis-Duphil, Michele; Mathien-Shire, Yolande; Herve, Guy
CS Lab. Enzymol., CNRS, Gif-sur-Yvette, 91190, Fr.
SO Journal of Bacteriology (1981), 148(2), 659-69 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB When a uracil- ***auxotrophic*** ***yeast*** strain is grown under uracil-limiting conditions, the aspartate transcarbamylase activity found in crude exts. shows a variation in sensitivity to feedback inhibition by UTP. This variation was correlated with changes in the mol. form of the carbamyl phosphate synthetase-uracil-aspartate transcarbamylase complex. Carbamyl phosphate synthetase-uracil (mol. wt. 240,000) and UTP-insensitive aspartate transcarbamylase (mol. wt. 140,000) were ***present*** sep. in exts. from cells collected in the early exponential phases, which contrasted with the ***presence*** of a single high-mol.-wt. form (mol. wt. .apprx.900,000) bearing both activities in exts. from stationary-phase cells. The lack of sensitivity to UTP by aspartate transcarbamylase was delayed by adding UTP before cell disruption and was prevented completely by adding phenylmethylsulfonyl fluoride. Thus, this event was attributed to a transient serine protease activity detected only in early exponential-phase cell exts. However, even in the ***presence*** of phenylmethylsulfonyl fluoride, a sucrose d. gradient anal. in the ***absence*** of UTP revealed a change in the aggregation state of the complex which might have occurred in vivo. None of these events was obsd. in exts. from cells that lacked protease B activity (strain HP232-2B).
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L17 ANSWER 140 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1981:546992 CAPLUS <<LOGINID::20100917>>
DN 95:146992
OREF 95:24549a,24552a
TI Genetic complementation of the Saccharomyces cerevisiae leu2 gene by the Escherichia coli leuB gene
AU Storms, Reginald K.; Holowachuck, Eugene W.; Friesen, James D.
CS Dep. Biol., York Univ., Downsview, ON, M3J 1P3, Can.
SO Molecular and Cellular Biology (1981), 1(9), 836-42 CODEN: MCEBD4; ISSN: 0270-7306
DT Journal
LA English
AB The leucine operon of E. coli was cloned on a plasmid possessing both E. coli and S. cerevisiae replication origins. This plasmid, pEH25, transformed leuA, leuB, and leuD auxotrophs of E. coli to prototrophy; it also transformed leu2 ***auxotrophs*** of S. ***cerevisiae*** to prototrophy. .beta.-Isopropylmalate dehydrogenase was encoded by the leuB gene of E. coli and the leu2 gene of yeast. Verification that the leuB gene ***present*** on pEH25 was responsible for complementing yeast leu2 was obtained by isolating, in E. coli, several leuB mutations that resided on the plasmid. These mutant leuB- plasmids were no longer capable of complementing leu2 in S. cerevisiae. Thus, S. cerevisiae can transcribe at least a portion of the polycistronic leu operon of E. coli and can translate a functional protein from at least the 2nd gene of this operon. The yeast Leu+ transformants obtained with pEH25, when cultured in minimal medium lacking leucine, grew with a doubling time 3-4-fold longer than when cultured in medium supplemented with leucine.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L17 ANSWER 141 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1981:403232 CAPLUS <<LOGINID::20100917>>
DN 95:3232
OREF 95:659a,662a
TI Metabolism of myoinositol during sporulation of myoinositol-requiring Saccharomyces cerevisiae
AU Schroeder, Renne; Breitenbach, Michael
CS Inst. Allgemeine Biochem. Ludwig Boltzmann-Forschungsstelle Biochem., Vienna, A-1090, Austria
SO Journal of Bacteriology (1981), 146(2), 775-83 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB Sporulation was studied in diploid S. ***cerevisiae*** strains homozygous for inositol ***auxotrophic*** markers. The strains required different amts. of inositol for the completion of sporulation. Shift expts. revealed 2 phases of inositol requirement during sporulation which coincide with 2 phases of lipid synthesis. Phase I was at the beginning and during premeiotic DNA synthesis; phase II immediately preceded the appearance of mature asci. Of the inositol taken up by sporulating cells, 90% was incorporated into inositol phospholipids. By 2-dimensional TLC, 8 compds. were resolved, 1 of which was sporulation-specific. The majority of the inositol phospholipids were identical to those found in vegetatively growing cells. In the ***absence*** of inositol, the cells did not sporulate but, after a certain time, were unable to return to vegetative growth. These nonsporulating cells incorporated acetate into lipids and doubled their DNA content in the premeiotic phase. Perhaps this lack of coordination of biosynthetic events causes inositolless death on sporulation media without inositol.
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L17 ANSWER 142 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1981:403179 CAPLUS <<LOGINID::20100917>>
DN 95:3179
OREF 95:647a,650a
TI Induction of choline transport and its role in the stimulation of the incorporation of choline into phosphatidylcholine by polyamines in a polyamine ***auxotroph*** of ***Saccharomyces*** ***cerevisiae***
AU Hosaka, Kohei; Yamashita, Satoshi
CS Sch. Med., Gunma Univ., Maebashi, 371, Japan
SO European Journal of Biochemistry (1981), 116(1), 1-6 CODEN: EJBCAI; ISSN: 0014-2956
DT Journal
LA English
AB A mutant of S. cerevisiae that was defective in ornithine decarboxylase was isolated. A prolonged culture of the mutant in a polyamine-free medium resulted in a decrease in the polyamine content and in cessation of growth. The addn. of polyamines to the culture induced growth after a lag of 5-6.5 h. The growth rate in the ***presence*** of polyamine was comparable to that of the wild-type strain. The effectiveness of polyamines was: spermidine > putrescine .apprxeq. spermine. Phosphatidylcholine-synthesizing activity during lag phase was detd. by measuring the incorporation of [14C]choline into phosphatidylcholine. The incorporation rate was increased with time by polyamine prior to the initiation of cell division.

Polyamines were effective in the following order: spermidine > putrescine .apprxeq. spermine. Expts. with methylglyoxal bis(guanylhydrazone), an inhibitor of S-adenosylmethionine decarboxylase, showed that putrescine stimulates cell growth and choline incorporation into phosphatidylcholine after it has been converted into spermidine in the cell. Induction of the choline transport system was responsible for the increase in the rate of incorporation of [14C]choline into phosphatidylcholine effected by polyamines. Cycloheximide prevented the induction of choline transport by polyamines. The levels of the CDP-choline pathway enzymes, such as choline kinase, cholinephosphate cytidyltransferase, and cholinephosphotransferase, were not significantly changed.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L17 ANSWER 143 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1981:80097 CAPLUS <<LOGINID::20100917>>
DN 94:80097
OREF 94:13011a,13014a
TI Control of recombination within and between DNA plasmids of Saccharomyces cerevisiae
AU Dobson, Melanie J.; Futcher, A. Bruce; Cox, Brian S.
CS Bot. Sch., Oxford, OX1 3RA, UK
SO Current Genetics (1980), 2(3), 193-200 CODEN: CUGED5; ISSN: 0172-8083
DT Journal
LA English
AB The [2 .mu.m+] leucine ***auxotroph*** of S. ***cerevisiae*** MC16 and the [2 .mu.m0] leucine ***auxotroph*** of S. carlsbergensis CB11 were transformed to prototrophy with plasmid pJDB219, which contains the 2-.mu.m yeast plasmid DNA, the yeast nuclear LEU2+ gene, and the ColE1 deriv. pMB9. In the [2 .mu.m+] transformants, a new plasmid (+YX) was generated, probably by recombination between pJDB219 and 2-.mu.m DNA. In the ***absence*** of 2-.mu.m DNA, pYX existed in equimolar amts. of 2 forms (A and B), which probably arose by intramol. recombination across the inverted repeats of the 2-.mu.m portion of pYX. Plasmid pJDB219 required the ***presence*** of 2-.mu.m DNA to undergo intramol. recombination. Apparently, 2-.mu.m DNA and pYX code for a gene product required for this recombination event which pJDB219 cannot produce.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L17 ANSWER 144 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1981:80082 CAPLUS <<LOGINID::20100917>>
DN 94:80082
OREF 94:13011a,13014a
TI Transformation of Saccharomyces cerevisiae with plasmids containing fragments of yeast 2 .mu. DNA and a suppressor tRNA gene
AU Thomas, David Y.; James, Allen P.
CS Div. Biol. Sci., Natl. Res. Counc. Canada, Ottawa, ON, K1A OR6, Can.
SO Current Genetics (1980), 2(1), 9-16 CODEN: CUGED5; ISSN: 0172-8083
DT Journal
LA English
AB Hybrid plasmids were constructed which contained segments of the yeast plasmid 2 .mu. DNA, the yeast ochre-suppressing SUP4.0 gene, and the bacterial plasmid pBR322. ***Yeast*** transformation is detected with a host contg. multiple ochre ***auxotrophic*** mutations. The transformed SUP4.0 gene is active and can promote growth in the ***absence*** of all the requirements. Plasmids contg. different fragments of 2 .mu. DNA all appear to be active in high frequency transformation of yeast contg. 2 .mu. DNA, except those contg. the HindIII-D fragment. The transforming plasmids undergo recombination with the indigenous 2 .mu. DNA. Integration of the transforming plasmid into the host chromosome was detected by hybridization of restriction enzyme cleaved DNA with labeled pBR322. The plasmids contain restriction enzyme sites which can be used for cloning other genes into yeast.

L17 ANSWER 145 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1981:27284 CAPLUS <<LOGINID::20100917>>
DN 94:27284
OREF 94:4477a,4480a
TI Incorporation of algal thylakoid membrane and DNA in yeast protoplasts
AU Kawakami, N.; Tanaka, H.; Mondo, H.; Katamine, S.; Kawakami, H.
CS Fac. Eng., Hiroshima Univ., Hiroshima, 730, Japan
SO Symposia Biologica Hungarica (1980), Volume Date 1979, 22(Adv. Protoplast Res.), 49-54 CODEN: SYBHAK; ISSN: 0082-0695
DT Journal
LA English
AB Protoplasts of an adenine ***auxotroph*** of ***Saccharomyces*** ***cerevisiae*** were strongly aggregated with isolated thylakoid membranes of the blue-green alga Anabaena cylindrica or chloroplasts of the green alga Chlorella ellipsoidea in the ***presence*** of polyethylene glycol 7500. The photosynthetic structures were often incorporated into vacuoles of the protoplasts as fragments or disintegrated materials. No intact algal photosynthetic organelle was obsd. in the yeast protoplasts with the electron microscope. DNA isolated from A. cylindrica or C. ellipsoidea was also taken up by the yeast protoplasts, sometimes resulting in the formation of yeast prototrophs at low frequency. Perhaps contaminating DNA from S. carlsbergensis in the enzyme prepn. used to induce protoplast formation by S. cerevisiae was actually responsible for repair of the ade marker.

L17 ANSWER 146 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1980:634879 CAPLUS <<LOGINID::20100917>>
DN 93:234879
OREF 93:37555a,37558a
TI The Herpes Simplex virus thymidine kinase gene is not expressed in Saccharomyces cerevisiae
AU Kiss, G. B.; Cornish, K. V.; Pearlman, R. E.; Friesen, J. D.
CS Dep. Biol., York Univ., Downsview, ON, M3J 1P3, Can.
SO Recombinant DNA Technical Bulletin (1980), 3(1), 21-4 CODEN: RDTBD5; ISSN: 0196-0229
DT Journal
LA English
AB The herpes simplex virus (HSV) thymidine kinase (tk) gene, carried on a BamHI fragment that had been cloned on plasmid pBR322, was cloned on the chimeric S. cerevisiae plasmid pVF91. The plasmid (pGY14) thus constructed contained a 3.6-kilobase-pair (kbp) fragment of the yeast 2 .mu.m circle, a 6.0-kbp fragment with the yeast leu2 gene, almost all of the Escherichia coli pBR322 plasmid, and the 3.4-kbp fragment with the HSV tk gene. Plasmid pGY14 was used to transform a leucine ***auxotroph*** of S. ***cerevisiae*** . The ***presence*** of pGY14 in a Leu+ transformant (designated

GY700) was verified by isolating DNA from the strain and using it to transform E. coli, selecting for ampicillin resistance (encoded by pBR322). Various data indicated that the HSV tk gene in GY700 could be transcribed, but the RNA was not polyadenylated nor translated either as a functional or antigenically cross-reacting protein.

L17 ANSWER 147 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1979:520020 CAPLUS <<LOGINID::20100917>>
DN 91:120020
OREF 91:19333a,19336a
TI Peptidase activities in Saccharomyces cerevisiae
AU Rose, Bruce; Becker, Jeffrey M.; Naider, Fred
CS Dep. Chem., City Univ. New York, Staten Island, NY, 10301, USA
SO Journal of Bacteriology (1979), 139(1), 220-4 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB At least 4 distinct aminopeptidase activities and a single dipeptidase activity were found in cell exts. of a leucine-lysine ***auxotroph*** of S. ***cerevisiae*** . The assay for peptidase activity involved polyacrylamide gel electrophoresis followed by an enzyme-coupled activity staining procedure. The aminopeptidases had largely overlapping specificities but could be distinguished from one another by their electrophoretic mobilities and activities toward different peptide substrates. Substrates ***tested*** included both free and blocked di- and tripeptides and amino acid derivs.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L17 ANSWER 148 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1979:471614 CAPLUS <<LOGINID::20100917>>
DN 91:71614
OREF 91:11537a,11540a
TI Isolation and preliminary characterization of ***Saccharomyces*** ***cerevisiae*** proline ***auxotrophs***
AU Brandriss, Marjorie C.
CS Dep. Biol., Massachusetts Inst. Technol., Cambridge, MA, 02139, USA
SO Journal of Bacteriology (1979), 138(3), 816-22 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB Proline-requiring mutants of S. cerevisiae were isolated. Each mutation was recessive and was inherited as expected for a single nuclear gene. Three complementation groups could be defined which were believed to correspond to mutations in the 3 genes (pro1, pro2, and pro3) coding for the 3 enzymes of the pathway. Mutants defective in the pro1 and pro2 genes could be satisfied by arginine or ornithine as well as proline. This suggests that the blocks are in steps leading to glutamate semialdehyde, either in glutamyl kinase or glutamyl phosphate reductase. A pro3 mutant was shown by enzyme assay to be deficient in .DELTA.1-pyrroline-5-carboxylate reductase which converts pyrroline-5-carboxylate to proline. A unique feature of ***yeast*** proline ***auxotrophs*** is their failure to grow on the rich medium, ***yeast*** ext.-peptone-glucose. This failure is not understood at ***present*** , although it accounts for the ***absence*** of proline auxotrophs in previous screening for amino acid auxotrophy.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)

L17 ANSWER 149 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1979:164482 CAPLUS <<LOGINID::20100917>>
DN 90:164482
OREF 90:26075a
TI Synthesis and activation of asparagine in asparagine ***auxotrophs*** of ***Saccharomyces*** ***cerevisiae***
AU Ramos, Fernando; Wiame, Jean Marie
CS Fac. Sci., Univ. Libre Bruxelles, Brussels, Belg.
SO European Journal of Biochemistry (1979), 94(2), 409-17 CODEN: EJBCAI; ISSN: 0014-2956
DT Journal
LA English
AB ***Tests*** of cofactors in cell-free exts. showed that L-asparagine synthesis in S. cerevisiae is performed by a glutamine-dependent asparagine synthetase of the type found in higher organisms. Auxotrophy for asparagine was obtained in 2 classes of mutants. In class I, asparagine synthetase activity is cancelled. These mutants combine 2 mutations, asnA and asnB. Neither mutation alone gives total auxotrophy. Partial auxotrophy and a strong decrease in enzyme activity result from asnA mutation. No change is detectable in cells with the asnB mutation alone. This, and G. E. Jones' report (1978) of auxotrophy resulting from the combination of 2 mutations, show asparagine synthesis to be an unusual biosynthetic operation. In class II, auxotrophy results from a single mutation which modifies the efficiency of the asparaginyl-tRNA synthetase (asnRS mutation). This auxotrophy is cancelled if asparaginase I activity (the only 1 ***present*** in the given wild type) is cancelled by a casnI mutation. This latter mutation allows an increase in the asparagine pool which is able to compensate for the asparaginyl-tRNA synthetase partial defect of the asnRS mutant.
OSC.G 9 THERE ARE 9 CAPLUS RECORDS THAT CITE THIS RECORD (9 CITINGS)

L17 ANSWER 150 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1979:117978 CAPLUS <<LOGINID::20100917>>
DN 90:117978
OREF 90:18627a,18630a
TI Isolation and characterization of ***yeast*** mutants ***auxotrophic*** for 2'-deoxythymidine 5'-monophosphate
AU Little, J. G.; Haynes, R. H.
CS Dep. Biol., York Univ., Toronto, ON, Can.
SO Molecular and General Genetics (1979), 168(2), 141-51 CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB Mutant strains of ***Saccharomyces*** ***cerevisiae*** ***auxotrophic*** for TMP were isolated and characterized. Two distinct classes of auxotrophs were obtained. One class had a simple requirement for TMP and was analogous to thymine-requiring bacteria. The 2nd class required TMP, adenine, histidine, and methionine; this complex nutritional phenotype was due to defects in folate metab. The TMP-dependent growth of respiratory-competent grande auxotrophs was markedly affected by medium compn. and C source. In the ***absence*** of TMP thymineless death occurred in both mutant classes.
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)

L17 ANSWER 151 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1978:611739 CAPLUS <<LOGINID::20100917>>
DN 89:211739
OREF 89:32867a,32870a
TI Hybrid analysis of morphological mutants in Saccharomyces cerevisiae, which produce pseudomycelial cells
AU Le Dinh Luong; Egorova, V. N.; Inge-Vechtomov, S. G.
CS Dep. Genet. Breed., A. A. Zhdanov State Univ. Leningr., Leningrad, USSR
SO Genetika (Moscow) (1978), 14(9), 1552-63 CODEN: GNKAA5; ISSN: 0016-6758
DT Journal
LA Russian
AB Crossing of Rpm (rough pseudomycelial) mutants of S. ***cerevisiae*** with morphol. normal nutritional ***auxotrophs*** gave smooth colonies, indicating the recessive nature of rpm mutations. Complementation ***tests*** showed the ***presence*** of 3 genes, rpm 1, rpm 2, and rpm 3, unlinked with each other or with the other markers. Tetrad anal. also showed most of the mutations to be monogenic and suggested that rpm 1 and rpm 3 might be linked with centromeres. All 3 mutations produce linear asci in homozygotes; heterozygotes give linear asci if the diploids are preincubated on grape juice medium, a medium which also gives elongation of vegetative cells.

L17 ANSWER 152 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1978:402895 CAPLUS <<LOGINID::20100917>>
DN 89:2895
OREF 89:531a,534a
TI Polyamine ***auxotrophs*** of ***Saccharomyces*** ***cerevisiae***
AU Whitney, Patricia A.; Morris, David R.
CS Dep. Biochem., Univ. Washington, Seattle, WA, USA
SO Journal of Bacteriology (1978), 134(1), 214-20 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB Strains of yeast were constructed that were unable to synthesize ornithine and were thereby deficient in polyamine biosynthesis. These strains were used to develop a protocol for isolation of mutants blocked directly in polyamine synthesis. There were 7 mutants isolated that lack ornithine decarboxylase activity; these strains exhibited decreased pool levels of putrescine, spermidine, and spermine when grown in the ***absence*** of polyamines. Three of the mutants lack S-adenosylmethionine decarboxylase activity; polyamine limitation of a representative mutant resulted in an accumulation of putrescine and a decrease in spermidine and spermine. When the mutants were cultured in the ***absence*** of polyamines, a continuously declining growth rate was obsd.
OSC.G 5 THERE ARE 5 CAPLUS RECORDS THAT CITE THIS RECORD (5 CITINGS)

L17 ANSWER 153 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1978:101331 CAPLUS <<LOGINID::20100917>>
DN 88:101331
OREF 88:15853a,15856a
TI Nucleoside Y metabolism in a ***Saccharomyces*** ***cerevisiae*** guanine ***auxotroph*** , (gua2 su+)
AU Lacharme, J.; Seigle-Murandi, F.; Steiman, R.
CS Lab. Biol. Veg. Cryptogam., UER Pharm., Meylan, Fr.
SO Comptes Rendus des Seances de la Societe de Biologie et de Ses Filiales (1977), 171(4), 814-17 CODEN: CRSBAW; ISSN: 0037-9026
DT Journal
LA French
AB Concns. of nucleoside Y (I), a guanosine deriv., and phenylalanine tRNA (II), which contains I, were followed in batch cultures of a haploid S. ***cerevisiae*** guanine ***auxotroph*** pulse-labeled with guanine-14C. The sp. activity of free I was higher than that of I isolated from II, which implies that I is synthesized independently and incorporated into II, and does not result from modification of guanosine already ***present*** in II. Internal concns. of I (free and bound) and II were both highest in lag-phase cells (8 h after inoculation) and fell during logarithmic growth (15-30 h after inoculation). This time course implies that free I may be a mitogen. At least part of the drop in the intracellular concn. of I was due to excretion, as the extracellular concn. of I-14C was highest at 25 h.

L17 ANSWER 154 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1978:2890 CAPLUS <<LOGINID::20100917>>
DN 88:2890
OREF 88:535a,538a
TI Developmental defects associated with glucosamine ***auxotrophy*** in ***Saccharomyces*** ***cerevisiae***
AU Ballou, Clinton E.; Maitra, Shyamal K.; Walker, Jeffery W.; Whelan, William L.
CS Dep. Biochem., Univ. California, Berkeley, CA, USA
SO Proceedings of the National Academy of Sciences of the United States of America (1977), 74(10), 4351-5 CODEN: PNASA6; ISSN: 0027-8424
DT Journal
LA English
AB S. cerevisiae mutants, unable to make D-glucosamine (I) due to a defect in 2-amino-2-deoxy-D-glucose-6-phosphate ketol-isomerase (amino-transferring) (EC 5.3.1.19), showed aberrations both in sporulation and in vegetative growth. They grew normally on a medium of yeast ext., peptone, and dextrose (YEPD) contg. I (1 mg/mL), and such cells accumulated 4-5-fold the amt. of I ***present*** in wild-type cells cultured on YEPD alone. When such mutant cells were shifted to YEPD alone, they continued to increase in cell mass for 3-4 cell cycles and produced strings of beads in which the cells failed to sep. Septation was defective apparently due due to the inability to synthesize chitin, which forms the primary septum in S. cerevisiae. The viability of such cultures dropped rapidly after 3-5 h owing to lysis of the cells through wall defects in the septum region. When the mutant cells grown on YEPD plus I were transferred to sporulation medium (1% KOAc), they produced viable spores altered only in the nature of the spore wall. The spores lacked a dark-staining surface layer visible in thin sections prepd. from wild-type cells, they were less hydrophobic than wild-type spores, and they were digested and lysed by glucanases that do not affect normal spores. All of these properties suggest that I is required for spore maturation and is used to synthesize a glucanase-resistant hydrophobic surface layer on the primary glucan spore wall. I synthesis and the activity of the isomerase did not appear until late in meiosis when tetranucleate cells were abundantly ***present*** in the sporulation culture.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)

L17 ANSWER 155 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1977:597139 CAPLUS <<LOGINID::20100917>>
DN 87:197139
OREF 87:31171a,31174a
TI Characteristics of ultraviolet light-induced ***auxotrophs*** in ***Saccharomyces*** ***cerevisiae***
AU Liu, Daniel S. H.
CS Dep. Chem., Illinois State Univ., Normal, IL, USA
SO Transactions of the Illinois State Academy of Science (1976), 69(3), 336-43 CODEN: TISAAH; ISSN: 0019-2252
DT Journal
LA English
AB UV-induced ***auxotrophs*** of S. ***cerevisiae*** S288C were studied by reversion ***tests*** with ICR-170, N-methyl-N'-nitro-N-nitrosoquanidine, Et methanesulfonate, and UV. The results show that UV produces both base-pair substitution and frameshift mutations in this eukaryote. In addn., some mutants are reverted strongly by UV but not by the chem. mutagens used.

L17 ANSWER 156 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1977:463539 CAPLUS <<LOGINID::20100917>>
DN 87:63539
OREF 87:10067a,10070a
TI The use of yeast cultures for the detection of environmental mutagens using a fluctuation ***test***
AU Parry, James M.
CS Dep. Genet., Univ. Coll. Swansea, Swansea, UK
SO Mutation Research, Environmental Mutagenesis and Related Subjects (1977), 46(3), 165-75 CODEN: MEMSE8
DT Journal
LA English
AB A microbial fluctuation ***test*** , modified for the detection of environmental mutagens was evaluated using a no. of strains of the yeast Saccharomyces cerevisiae. ***Auxotrophic*** diploid cultures of ***yeast*** which produce prototrophic colonies by both mitotic gene conversion and mutation have been extensively utilized for the detection and evaluation of chems. showing genetic activity. A no. of the yeast strains utilized were shown to be suitable for use in the fluctuation ***test*** although the time scales of the expts. were considerably extended (up to 16 days) compared to those involving bacteria. The yeast strains respond to doses of mutagens at least a 100-fold lower than that required in a conventional short exposure treat and plate expt. In expts. involving the induction of mitotic gene conversion at the tryptophan-5 and histidine-4 loci in the fluctuation ***test*** significant increases in prototrophic cells were produced in the ***presence*** of the insecticide Lindex [58-89-9] (0.05 .mu.g/mL), the preservative thiomersal [54-64-8] (0.0001 .mu.g/mL), a mahogany hair dye (0.01 .mu.g/mL), the herbicide paraquat [4685-14-7] (0.02 .mu.g/mL) and the alkylating agent ethyl methanesulfonate [62-50-0] (0.1 .mu.g/mL). The results demonstrate that the fluctuation ***test*** provides an extremely sensitive assay for the detection of chems. which show genetic activity in yeast at nontoxic concns.
OSC.G 4 THERE ARE 4 CAPLUS RECORDS THAT CITE THIS RECORD (4 CITINGS)

L17 ANSWER 157 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1977:151642 CAPLUS <<LOGINID::20100917>>
DN 86:151642
OREF 86:23783a,23786a
TI Studies of energy linked reactions: a cofactor function for unsaturated fatty acids in oxidative phosphorylation; studies with a ***yeast*** ***auxotroph***
AU Griffiths, David E.; Hyams, Robert L.; Bertoli, Enrico; Carver, Mark
CS Dep. Mol. Sci., University of Warwick, Coventry, UK
SO Biochemical and Biophysical Research Communications (1977), 75(2), 449-56 CODEN: BBRCA9; ISSN: 0006-291X
DT Journal
LA English
AB Mitochondria from a ***yeast*** unsatd. fatty acid ***auxotroph*** when grown with a high unsatd. fatty acid supplement catalyzed normal oxidative phosphorylation and dihydrolipoate-dependent ATP synthesis in the ***absence*** of added cofactors. Mitochondria from unsatd. fatty acid-depleted cells had half the unsatd. fatty acid content of supplemented cells and did not catalyze oxidative phosphorylation and dihydrolipoate-dependent ATP synthesis. Dihydrolipoate-dependent ATP synthesis was restored specifically by the addn. of cofactor amts. of oleic acid and oleoyl CoA. The results provide further evidence for a cofactor role for an unsatd. fatty acid in oxidative phosphorylation.

L17 ANSWER 158 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1976:589116 CAPLUS <<LOGINID::20100917>>
DN 85:189116
OREF 85:30245a,30248a
TI Yeast aspartate-dependent mutants which accumulates red pigment
AU Inge-Vechtomov, S. G.
CS Leningr. Gos. Univ. im. Zhdanova, Leningrad, USSR
SO Genetika (Moscow) (1976), 12(9), 50-60 CODEN: GNKAA5; ISSN: 0016-6758
DT Journal
LA Russian
AB Nineteen aspartate-requiring mutants were identified among 55 red mutants belonging to a haploid strain of Saccharomyces cerevisiae. The remaining 36 mutants required adenine. A mixt. of adenine, methionine, and threonine could substitute for aspartic acid in the stimulation of the growth of these mutants. All of the aspartate auxotrophs show a degree of leakiness. The growth of these mutants on minimal medium or in the ***presence*** of suboptimal aspartate concns. is inhibited by the ***presence*** of methionine, threonine, uracil, or arginine. Adenine stimulates growth. Three complementation groups are found, 2 of which are nonoverlapping. The function of these genes is discussed.

L17 ANSWER 159 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1976:519470 CAPLUS <<LOGINID::20100917>>
DN 85:119470
OREF 85:19185a,19188a
TI ***Yeast*** cell-cycle mutant cdc21 is a temperature-sensitive thymidylate ***auxotroph***
AU Game, J. C.
CS Div. Microbiol., Natl. Inst. Med. Res., London, UK
SO Molecular and General Genetics (1976), 146(3), 313-15 CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB Genetic ***tests*** with the yeast cell-cycle mutant cdc21 isolated by L. H. Hartwell indicate that the CDC21 gene in yeast is the same as the TMP1 gene, whose mutant alleles confer

an auxotrophic requirement for dTMP. Yeast strains carrying cdc21 can grow at 37.degree. in the ***presence*** of dTMP provided that they are permeable to this compd. The gene is linked to ade2 on chromosome XV, and a case of intragenic complementation between cdc21 and another tmp1 allele is reported.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L17 ANSWER 160 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1976:414595 CAPLUS <<LOGINID::20100917>>
DN 85:14595
OREF 85:2337a,2340a
TI Indirect selection for ***auxotrophic*** mutants of ***Saccharomyces*** ***cerevisiae*** using the antibiotic netropsin
AU Young, James D.; Gorman, John W.; Gorman, Jessica A.; Bock, Robert M.
CS Lab. Mol. Biol., Univ. Wisconsin, Madison, WI, USA
SO Mutation Research (1976), 35(3), 423-7 CODEN: MUREAV; ISSN: 0027-5107
DT Journal
LA English
AB The small basic oligopeptide antibiotic, netropsin [554-32-5], can be successfully employed as an effective counterselecting agent in S. cerevisiae. The use of the drug results in approx. 35-fold enrichment of ***auxotrophic*** mutants in a mutagenized culture of ***yeast*** . The exptl. procedure is quite simple and less time consuming than other ***presently*** used methods for indirect mutant selection in yeast.

L17 ANSWER 161 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1976:56350 CAPLUS <<LOGINID::20100917>>
DN 84:56350
OREF 84:9265a,9268a
TI Requirements for unsaturated fatty acids for the induction of respiration in Saccharomyces cerevisiae
AU Walenga, Ronald W.; Lands, William E. M.
CS Dep. Biol. Chem., Univ. Michigan, Ann Arbor, MI, USA
SO Journal of Biological Chemistry (1975), 250(23), 9130-6 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB Unsatd. fatty acids provided during the release from glucose repression were shown to be essential for derepression of respiration in an unsatd. fatty acid ***auxotroph*** of S. ***cerevisiae*** . Cells derepressed in the ***presence*** of oleic acid contained 3-6 times as much cytochrome per cell as those derepressed in the ***absence*** of unsatd. fatty acid or those derepressed with eicosaenoic acid. The .DELTA.9 isomer was the most efficient of the cis-octadecenoic acid isomers in supporting that increase, and eicosaenoic acid supported an increase at only 15% the rate obsd. with oleic acid. Derepression, even in the ***presence*** of oleic acid, proceeded only after a lag of 3 hr. When glucose was removed prior to the addn. of oleate, the lag was reduced by the time of the preincubation with glycerol. This result suggests that some processes necessary for increased respiration can proceed in the ***absence*** of an added unsatd. fatty acid, but these processes apparently require certain levels of unsatd. acids in the pre-existing lipids, since they occurred in cells whose membranes contained 50 mole % oleate, but not in cells contg. only 20 mole %. These processes leading to eventual increased respiration were inhibited by cycloheximide but not chloramphenicol, suggesting that protein synthesis on cytoplasmic ribosomes but not mitochondrial ribosomes was required. Derepression in the ***absence*** of oleate for 3 hr lessened the inhibition of respiration induction by ethidium bromide. This result indicates that the transcription of mitochondrial DNA necessary for the induction of respiration may have occurred in the ***absence*** of added unsatd. fatty acid, but that some subsequent event required added esterified unsatd. fatty acid.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

L17 ANSWER 162 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1975:575337 CAPLUS <<LOGINID::20100917>>
DN 83:175337
OREF 83:27533a,27536a
TI Methionine biosynthesis in ***Saccharomyces*** ***cerevisiae*** . I. Genetical analysis of ***auxotrophic*** mutants
AU Masselot, Monique; De Robichon-Szulmajster, Huguette
CS Lab. Enzymol., CNRS, Gif-sur-Yvette, Fr.
SO Molecular and General Genetics (1975), 139(2), 121-32 CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB In order to analyze how many structural genes are implicated in the specific steps of the synthesis of methionine in S. cerevisiae, a hundred mutants were studied by complementation. Twenty one groups were defined named MET1 to MET25. Neither recombination between independent mutants of the same complementation group nor linkage between different groups was found. Preliminary to biochem. studies, mutants of each complementation group were ***tested*** for their capacity to utilize various precursors of methionine.
OSC.G 15 THERE ARE 15 CAPLUS RECORDS THAT CITE THIS RECORD (15 CITINGS)

L17 ANSWER 163 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1975:528597 CAPLUS <<LOGINID::20100917>>
DN 83:128597
OREF 83:20207a,20210a
TI Nutrition and taxonomy of Enterobacteriaceae and related bacteria. I. Technical procedure for auxanograms
AU Veron, M.
CS Lab. Bacteriol., Fac. Med. Necker, Paris, Fr.
SO Annales de Microbiologie (Paris) (1975), 126A(3), 267-74 CODEN: ANMBCM; ISSN: 0300-5410
DT Journal
LA French
AB The nutritional requirements of 186 strains of Enterobacteriaceae were studied using an auxanographic method which, in contrast to methods in which media are supplemented with each substrate, involves diffusion of 146 substrates as sole sources of C and energy into media without an energy substrate. Sometimes large colonies form, but frequently one can observe microcolonies under a stereomicroscope. Some substrates have an inhibitory effect. With certain bacterial-substrate combinations, circular zones of growth were not obsd. but mutant colonies formed. Introduction of ***yeast*** ext. into the base media permitted comparison of phototrophic and ***auxotrophic*** strains under the same conditions. Most phototrophic strains of Enterobacteriaceae used more substrates in these media than in media without yeast ext., even though

growth is insignificant in the ***absence*** of other energy substrates. The method permits a concn. gradient of each substrate to be established, causes few mutants to develop, does not require substrate sterilization by heat, neutralization of substrate pH, or high purifn. of the substrates and agar.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

L17 ANSWER 164 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1975:493674 CAPLUS <<LOGINID::20100917>>
DN 83:93674
OREF 83:14709a,14712a
TI Biogenesis of mitochondria. 38. Effects of altered steady-state membrane lipid composition on mitochondrial-energy metabolism in Saccharomyces cerevisiae
AU Marzuki, Sangkot; Cobon, Gary S.; Haslam, J. M.; Linnane, Anthony W.
CS Dep. Biochem., Monash Univ., Clayton, Australia
SO Archives of Biochemistry and Biophysics (1975), 169(2), 577-90 CODEN: ABBIA4; ISSN: 0003-9861
DT Journal
LA English
AB A chemostat culture technique has been developed for the growth of an unsatd. fatty acid ***auxotroph*** of S. ***cerevisiae*** . Any chosen steady-state cellular unsatd. fatty acid level between 75 and 15% of the total fatty acids could be established and maintained. In all cultures the steady-state glucose concns. were maintained at levels below that which induces catabolite repression. The efficiency of oxidative phosphorylation as detd. from the M growth yield decreased as the cellular unsatd. fatty acid compn. was lowered. The no. of moles of ATP produced by oxidative phophorylation per mole of glucose utilized was 7.2, 4.8, 0.7, and 0.4 for cells in which 75, 50, 44, and 34% resp., of the total fatty acids were unsatd. The lesion in oxidative phosphorylation was a direct result of lowering the membrane unsatd. fatty acid compn. as the respiratory activities and cytochrome content of cells and mitochondria were unaffected by a decrease in the cellular unsatd. fatty acid level from the wild-type value of .apprx.75% down to .apprx.34%. In cells which contained lipids with 22-28% unsatd. fatty acids, cyanide-sensitive respiration was ***absent*** , and the levels of all mitochondrial cytochromes were <10% of normal. The redn. in the levels of cytochromes aa3 and b appeared to be a consequence of a loss of mitochondrial protein synthetic activity in such cells. The level of cytochrome c was also greatly decreased, indicating that the cellular unsatd. fatty acid compn. was affecting either the synthesis in the cytoplasm of mitochondrial proteins or the assembly of these proteins in the mitochondria.

L17 ANSWER 165 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1975:121444 CAPLUS <<LOGINID::20100917>>
DN 82:121444
OREF 82:19407a,19410a
TI Biosynthesis of lysine in Rhodotorula glutinis. Role of pipecolic acid
AU Kurtz, M.; Bhattacharjee, J. K.
CS Dep. Microbiol., Miami Univ., Oxford, OH, USA
SO Journal of General Microbiology (1975), 86, Pt. 1, 103-10 CODEN: JGMIAN; ISSN: 0022-1287
DT Journal
LA English
AB Glutamate-.alpha.-ketoadipate transaminase, saccharopine reductase, and saccharopine dehydrogenase activities were demonstrated in exts. of R. glutinis but .alpha.-aminoadipate reductase activity could not be measured in whole cells or in exts. Lysine auxotroph lys1 grew in the ***presence*** of L-lysine or DL-.alpha.-aminoadipate and incorporated radioacitivity from DL-.alpha.-aminoadipate-U-14C into lysine during growth. Growing wild-type cells converted L-lysine-U-14-C into .alpha.-aminoadipate-14C, suggesting both biosynthetic and degradative roles for .alpha.-aminoadipate. Lysine auxotrophs lys1, lys2, and lys3 of R. glutinis, unlike lysine ***auxotrophs*** of ***Saccharomyces*** cervisiae, satisfied their growth requirement with L-pipecolate. Moreover, exts. of wild-type R. glutinis catalyzed the conversion of L-pipecolate to .alpha.-aminoadipate-.delta.-semialdehyde. These results suggest a biosynthetic role for L-pipecolate in R. glutinis but not in S. cervisiae.

L17 ANSWER 166 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1975:40518 CAPLUS <<LOGINID::20100917>>
DN 82:40518
OREF 82:6439a,6442a
TI Thymineless death in a strain of ***Saccharomyces*** ***cerevisiae*** ***auxotrophic*** for deoxythymidine-5'-monophosphate
AU Brendel, Martin; Langjahr, Ursula G.
CS Fachbereich Biol., Johann Wolfgang Goethe-Univ., Frankfurt/Main, Fed. Rep. Ger.
SO Molecular and General Genetics (1974), 131(4), 351-8 CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB Cells of S. ***cerevisiae*** strain 211-1atmp1-1 which are ***auxotrophic*** for deoxythymidine-5'-monophosphate (5'-dTMP) exhibit thymineless death (TLD) when deprived of the nucleotide. After an initial lag of .apprx. 1 generation time, cells lose viability in exponential fashion halving their titer every 90 min. Thymine and thymidine (100 .mu.g/ml) cannot prevent TLD in the ***absence*** of 5'-dTMP. Although the cell titer is const. during 24 hr of 5'-dTMP deprivation, the cell mass increases by a factor of 6 during this period. Budding is stopped and cells attain a swollen shape. Synthesis of RNA and protein does occur in cells deprived of 5'-dTMP, the rate of synthesis being significantly lower than those in the controls.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L17 ANSWER 167 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1974:487766 CAPLUS <<LOGINID::20100917>>
DN 81:87766
OREF 81:13919a,13922a
TI Formation of higher alcohols by amino acid ***auxotrophic*** mutants of ***Saccharomyces*** ***cerevisiae*** . II. Influence of threonine, isoleucine, valine, and leucine
AU Vollbrecht, D.
CS Inst. Mikrobiol. Weinforsch., Johannes Gutenberg-Univ., Mainz, Fed. Rep. Ger.
SO Archives of Microbiology (1974), 97(2), 149-62 CODEN: AMICCW; ISSN: 0302-8933
DT Journal
LA German
AB Variation of amino acid uptake and degrdn. to higher alcs. as a function of amino acid concn. was studied in a mutant S. cerevisiae strain. Cell mass increased with increasing concn. of threonine, isoleucine, valine, and leucine, the latter 2 giving

higher dry wts. The amino acids were completely utilized when ***present*** at low concn., but up to 20% was not utilized when the concn. was high. The relative extent of uptake of each amino acid depended on its relative proportion in the medium, more being taken up as its proportion increased. The amino acids competed with each other for uptake by the cells. More intracellular isoleucine and leucine were converted to 2- and 3-methylbutanol than valine and threonine were converted to iso-BuOH and PrOH. The amino acids competed for degrdn. to the corresponding alcs.

L17 ANSWER 168 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1974:487082 CAPLUS <<LOGINID::20100917>>
DN 81:87082
OREF 81:13807a,13810a
TI Evidence for the identity of O-acetylserine sulfhydrylase with O-acetylhomoserine sulfhydrylase in yeast
AU Yamagata, Shuzo; Takeshima, Kazuhito; Naiki, Nobuo
CS Fac. Gen. Educ., Gifu Univ., Nagara, Japan
SO Journal of Biochemistry (1974), 75(6), 1221-9 CODEN: JOBIAO; ISSN: 0021-924X
DT Journal
LA English
AB O-Acetyl-L-homoserine (OAH) sulfhydrylase [37290-90-7] was highly purified from bakers' yeast by a modification of a previous method. When assayed in phosphate buffer, but not in Tris-HCl buffer, the purified enzyme catalyzed the O-acetyl-L-serine (OAS) sulfhydrylas [37290-89-4] reaction at a rate which was .apprx.15% that of the OAH sulfhydrylase reaction. The apparent ***absence*** of OAS sulfhydrylase activity in Tris-HCl buffer was found to be due to the instability of OAS in this buffer at alk. pH. Throughout the purifn. steps, the OAH and OAS sulfhydrylase activities were purified in parallel, and neither DEAE-cellulose column chromatog. of a partially purified prepn. nor Sepharose 4B gel filteration of the final prepn. could sep. the 2 activities. Upon polyacrylamide gel electrophoresis, the purified enzyme was sepd. into 3 protein bands, of which only the main band possessed the 2 activities. Moreover, the 2 activities behaved in the same way on heat treatment. Finally, the levels of OAS sulfhydrylase activity in exts. of various methionine ***auxotrophs*** of ***yeast*** varied in parallel with those of OAH sulfhydrylase activity. It is concluded that OAS and OAH sulfhydrylase activities of yeast are catalyzed by the same enzyme protein.
OSC.G 13 THERE ARE 13 CAPLUS RECORDS THAT CITE THIS RECORD (13 CITINGS)

L17 ANSWER 169 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1974:435463 CAPLUS <<LOGINID::20100917>>
DN 81:35463
OREF 81:5693a,5696a
TI Induction and complementation of lysine ***auxotrophs*** in ***Saccharomyces***
AU Biswas, G. D.; Bhattacharjee, J. K.
CS Dep. Microbiol., Miami Univ., Oxford, OH, USA
SO Antonie van Leeuwenhoek (1974), 40(2), 221-31 CODEN: ALJMAO; ISSN: 0003-6072
DT Journal
LA English
AB Four chem. agents as well as uv were used to induce mutations in the wild-type haploid strain X2180-1B (.alpha.) of Saccharomyces. A total of 2053 lysine-requiring mutant clones were isolated from many independent treatments and by nystatin enrichment technique. Mutants were classified into various functional groups on the basis of complementation anal. with 14 ***tester*** strains (lys 1 to lys 15 except lys 3). Of the clones analyzed, the nos. of isolates unable to complement with a given ***tester*** strain ranged from 2 for lys 5 to 918 for lys 4. Three of the mutually complementing lysine loci (lys 1, lys 2, and lys 4) accounted together for over 85% of the mutant clones whereas lys 6, lys 7, lys 8, and lys 14 had less than 10 noncomplementing isolates each. Mutants for lys 4 were most frequent with all of the mutagens ***tested*** except with HNO2 in which case the mutants for lys 2 were most frequent. A total of 56 isolates failed to complement with lys 10, lys 11, and lys 12. Similarly, 47 isolates failed to complement with lys 9 and lys 13 simultaneously. Only 44 isolates complemented with all of the ***tester*** strains used.

L17 ANSWER 170 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1974:142924 CAPLUS <<LOGINID::20100917>>
DN 80:142924
OREF 80:23057a,23060a
TI Association of methionine requirement with methyl mercury-resistant mutants of yeast
AU Singh, Arjun; Sherman, Fred
CS Sch. Med., Univ. Rochester, Rochester, NY, USA
SO Nature (London, United Kingdom) (1974), 247(5438), 227-9 CODEN: NATUAS; ISSN: 0028-0836
DT Journal
LA English
AB Complementation ***testing*** and genetic anal. of meiotic segregants of sporulated diploid cells, obtained by crossing normal ***Saccharomyces*** ***cerevisiae*** with any of 8 Me2Hg-resistant mutants which were ***auxotrophic*** for methionine, showed all 8 were allelic mutants. The met locus in these mutants was designated met15 as it segregated independently of all previously known genes in methionine biosynthesis. At a crit. concn. of Me2Hg the methionine requirement of the metuk mutants was partially or totally alleviated. A model for this interrelation of methionine requirement and Me2Hg resistance is proposed.
OSC.G 6 THERE ARE 6 CAPLUS RECORDS THAT CITE THIS RECORD (6 CITINGS)

L17 ANSWER 171 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1973:513121 CAPLUS <<LOGINID::20100917>>
DN 79:113121
OREF 79:18363a,18366a
TI Mutations affecting levels of tetrahydrofolate interconversion enzymes in Saccharomyces cerevisiae. I. Enzyme levels in ade3-41 and ADE15, a dominant adenine auxotroph
AU Lam, Keng-Bon; Jones, Elizabeth W.
CS Dep. Biol., Case West. Reserve Univ., Cleveland, OH, USA
SO Molecular and General Genetics (1973), 123(3), 199-208 CODEN: MGGEAE; ISSN: 0026-8925
DT Journal
LA English
AB A previously isolated adenine ***auxotroph*** mutant of S. ***cerevisiae*** which requires adenine was genetically investigated. The mutant was dominant to its wild type allele as measured by growth of the heterozygous diploid. The mutation resulted in altered levels of 3 tetrahydrofolate interconversion enzymes. It reduced the level of formyl tetrahydrofolic acid synthetase to 15% of the wild type specific activity, and elevated the levels of methenyl tetrahydrofolic acid cyclohydrolase and methylene tetrahydrofolic acid dehydrogenase. The ***presence*** of ade3-41 (which causes redn. in the levels of

the same 3 interconversion enzymes) in cis position to the ADE15 mutation eliminated dominance of the ADE15 mutation. Apparently the cis epistasis of ade3-41 to ADE15 results from both mutations lying in the same transcriptional unit.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L17 ANSWER 172 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1973:81965 CAPLUS <<LOGINID::20100917>>
DN 78:81965
OREF 78:13069a,13072a
TI Peptide utilization in ***yeast*** . Methionine and lysine ***auxotrophs*** of ***Saccharomyces*** ***cerevisiae***
AU Becker, Jeffrey M.; Naider, Fred; Katchalski, Ephraim
CS Dep. Biophys., Weizmann Inst. Sci., Rehovot, Israel
SO Biochimica et Biophysica Acta, Biomembranes (1973), 291(2), 388-97 CODEN: BBBMBS; ISSN: 0005-2736
DT Journal
LA English
AB A study was made of the growth response and cellular peptidase activity of several amino acid ***auxotrophs*** of S. ***cerevisiae*** to peptides contg. the required amino acid. A methionine-requiring auxotroph grew on and contained intracellular peptidase activity toward Met-Met, Met-Met-Met, and Met-Gly-Met-Met. In contrast, Gly-Met-Gly did not support the growth of this mutant nor did 3 lysine-requiring strains utilize any lysine-contg. peptides ***tested*** , although cell-free exts. from the respective mutants contained the necessary peptidase activity. The ***absence*** of a transport system of relatively high affinity for these peptides is suggested as the reason for their inability to satisfy the nutritional requirements of the cells.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L17 ANSWER 173 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1972:549516 CAPLUS <<LOGINID::20100917>>
DN 77:149516
OREF 77:24571a,24574a
TI Cystathionine synthesis in yeast. Alternative pathway for homocysteine biosynthesis
AU Savin, Michael A.; Flavin, Martin
CS Lab. Biochem., Natl. Heart Lung Inst., Bethesda, MD, USA
SO Journal of Bacteriology (1972), 112(1), 299-303 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB Cystathionine synthesis from O-acetylhomoserine and cysteine has been demonstrated in yeast exts. for the first time. The activity is less than that of O-acetylhomoserine sulfhydrylase, but it is higher than that reported for homoserine O-transacetylase and therefore should not be growth limiting. Cystathionine synthase seems to share the regulatory properties of the sulfhydrylase, and both activities are missing from the methionine ***auxotroph*** ***Saccharomyces*** ***cerevisiae*** EY9, suggesting that both reactions are catalyzed by the same enzyme. However, cystathionine synthase activity was lost during purification of the sulfhydrylase, suggesting that the two reactions may be catalyzed by sep. enzymes. Since previous studies have shown that yeast exts. can catalyze the cleavage of cystathionine to homocysteine, the ***present*** results show the existence of two complete alternate pathways for homocysteine biosynthesis in yeast.

OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L17 ANSWER 174 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1972:401221 CAPLUS <<LOGINID::20100917>>
DN 77:1221
OREF 77:251a,254a
TI Comparison of chemically induced reversion patterns of Salmonella typhimurium and Saccharomyces cerevisiae mutants, using in vitro plate ***tests***
AU Brusick, David J.; Zeiger, Errol
CS Div. Toxicol., Food Drug Adm., Washington, DC, USA
SO Mutation Research (1972), 14(3), 271-5 CODEN: MUREAV; ISSN: 0027-5107
DT Journal
LA English
AB Salmonella typhimurium and ***Saccharomyces*** ***cerevisiae*** ***auxotrophic*** mutants responded similarly to alkylating agents, in particular methyl methanesulfonate [66-27-3], nitrosomethylurea [684-93-5], nitrosomethylurethane [615-53-2], and nitrogen mustard [51-75-2], and to the acridine mustards ICR 170 [146-59-8] and ICR 191 [17070-44-9]. The base-pair substitution mutants of both organisms responded strongly to all the alkylating agents but were not reverted by the ICR compds. The frameshift mutants were distinguished from base-pair substitution mutants by their pos. responses to the acridines and(or) ICR compds.

L17 ANSWER 175 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1971:472889 CAPLUS <<LOGINID::20100917>>
DN 75:72889
OREF 75:11525a,11528a
TI Improvement in the nystatin ***test*** for the selection of mutants in Saccharomyces cerevisiae
AU Thouvenot, D. R.; Bourgeois, C. M.
CS Malt. Biochim. Appl., Ec. Super. Brass., Nancy, Fr.
SO Annales de l'Institut Pasteur (Paris) (1971), 120(5), 617-25 CODEN: AIPAAV; ISSN: 0020-2444
DT Journal
LA English
AB The efficacy of the method for selecting ***auxotrophic*** mutants of S. ***cerevisiae*** was improved by controlling the period of N starvation, the compn. of the culture medium, and the concn. of nystatin so that the lethal effect on the prototrophs and the enrichment effect on the auxotrophs were maximal. Thus adenine auxotrophs were induced in a medium contg. (NH4)2SO4 as N source and 150 units of nystatin per ml following a 24-hr period of N starvation. Ten different amino acid auxotrophs were isolated.

L17 ANSWER 176 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1971:136919 CAPLUS <<LOGINID::20100917>>
DN 74:136919
OREF 74:22083a,22086a
TI Leaky mutation and coordinate regulation of the accumulation of lysine-precursors in Saccharomyces
AU Bhattacharjee, Jnanendra K.
CS Dep. Microbiol., Miami Univ., Oxford, OH, USA
SO Canadian Journal of Genetics and Cytology (1970), 12(4), 785-9 CODEN: CNJGA8; ISSN: 0008-4093
DT Journal
LA English

AB Lysine ***auxotroph*** (ly 12) of ***Saccharomyces*** exhibited a residual ability (leakiness) to grow in minimal medium. It showed a submaximal growth with a long lag period in the minimal medium. The intermediates, characteristic of this mutant, were identified as homocitric, homoisocitric, and cis-homoaconitic acids both in ***presence*** and in ***absence*** of lysine. The percent accumulation of all 3 intermediates was reduced significantly and simultaneously in the ***presence*** of lysine as compared with the minimal medium: homocitric acid (38%), homoaconitic acid (31%), and homoisocitric acid (33%). The difference in redn. for the 3 intermediates was not significant.

L17 ANSWER 177 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1971:84313 CAPLUS <<LOGINID::20100917>>
DN 74:84313
OREF 74:13651a,13654a
TI Morphology, physiology, and virulence of some mutants of Candida albicans
AU Savage, Norman; Balish, Edward
CS Oak Ridge Assocd. Univ., Oak Ridge, TN, USA
SO Infection and Immunity (1971), 3(1), 141-8 CODEN: INFIBR; ISSN: 0019-9567
DT Journal
LA English
AB After induction of mutants of Candida albicans with UV light, N-methyl-N'-nitro-N-nitrosoguanidine (I), and N-nitroso-N-methylurethane (II), 1 methionine and 2 adenine ***auxotrophs*** exhibited ***yeastlike*** morphol. in complex media and had sugar fermentation patterns typical of C. albicans, and all were agglutinated by C. albicans antiserum. Chlamydospore production was ***absent*** in the nonpigmented adenine mutants, and the chlamydospores produced by the methionine auxotrophs were distorted. Germ tubes were formed in human serum by the auxotrophs and prototrophs. Virulence for mice was retained by all auxotrophs but generally at a reduced level. The methionine auxotroph, only slightly less virulent than the prototroph, was more virulent than a pigmented adenine mutant and a practically avirulent nonpigmented adenine auxotroph.

L17 ANSWER 178 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1970:401227 CAPLUS <<LOGINID::20100917>>
DN 73:1227
OREF 73:207a,210a
TI Influence of nitrate, chlorate, sulfate, form of iron oxide, and growth conditions on the extent of bacteriological reduction of iron
AU Ottow, J. C. G.
CS Inst. Landwirt. Mikrobiol., Justus-Liebig-Univ., Giessen, Fed. Rep. Ger.
SO Zeitschrift fuer Pflanzenernaehrung und Bodenkunde (1969), 124(3), 238-53 CODEN: ZPBOAL; ISSN: 0044-3263
DT Journal
LA German
AB The mechanism and ecol. significance was studied of the redn. of iron by bacteria, that are potentially capable of reducing ferric oxides into the sol. ferrous state. In addn., the influence of environmental factors such as soil and yeast ext., the type of iron oxide, the pH, and electron acceptors NO3-, ClO3-, and SO42- on the rate of iron redn. with some selected iron reducing bacteria has been detd. Depending on the prototrophic or ***auxotrophic*** nutrition of the bacteria ***tested***, addn. of soil or ***yeast*** ext. reduced and enhanced, resp., the amt. of dissolved ferrous iron. With increasing crystallinity of the iron compd. its reducibility decreased in the sequence FePO4.4H2O > Fe(OH)3 > .gamma.-FeO.OH > .alpha.-FeOOH > .alpha.-Fe2O3. Like nitrate redn., the redn. of iron oxide by bacteria is most intensive in the originally neutral and alk. pH of the nutrient broth. When nitrate, chlorate, or sulfate were added to the medium in increasing amts., only NO3- and ClO3-, but not SO42-, could reduce the iron-reducing capacity of the organisms ***tested***, provided the enzyme nitrate reductase was inducible. Among the bacteria detd. qual. on their iron reducing ability, 25 species belonging to the Enterobacteriaceae, Bacillaceae, Pseudomonadaceae, and Micrococcaceae were capable of reducing ferric oxide. All except 2 contained the enzyme nitrate reductase. At least 2 different iron reducing mechanisms may exist, in one the enzyme nitrate reductase could be involved. A hypothesis on the enzymic iron reduction is ***presented***. In this mechanism ferric iron is thought to participate as an alternative electron acceptor during respiration at conditions of low O tensions such as after flooding a soil.
OSC.G 8 THERE ARE 8 CAPLUS RECORDS THAT CITE THIS RECORD (8 CITINGS)

L17 ANSWER 179 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1970:39955 CAPLUS <<LOGINID::20100917>>
DN 72:39955
OREF 72:7323a,7326a
TI Purine metabolism and riboflavine formation in microorganisms. II. Purine metabolism and riboflavine synthesis by a purine-deficient auxotroph of Candida guilliermondii
AU Zur Nieden, K.; Fritsche, W.; Schlee, D.; Reinbothe, H.
CS Martin-Luther-Univ., Halle/Saale, Fed. Rep. Ger.
SO Acta Biologica et Medica Germanica (1969), 23(2), 235-43 CODEN: ABMGAJ; ISSN: 0001-5318
DT Journal
LA German
AB Aminoimidazole carboxamide, adenine, adenosine, AMP, hypoxanthine, inos ine, and IMP could be utilized for growth and for riboflavine synthesis by a purine-deficient auxotroph of C. guilliermondii. Guanine, guanosine, GMP, and xanthine were not utilized for growth or for flavinogenesis. The slow growth rate in unsupplemented medium indicates that the auxotroph is a leaky mutant (with a stimulatory purine requirement). Adenine, guanine, hypoxanthine, and xanthine were taken into the cell at about the same rate. Adenine uptake from the complete medium was inhibited by KCN, suggesting an active transport mechanism. Growth and riboflavine production of the ***yeast*** ***auxotroph*** responded to the adenine concn. of the medium, and guanine and xanthine had no stimulating effect upon riboflavine synthesis in the ***presence*** of growth-limiting amts. of adenine. Thus, in C. guilliermondii, adenine or more likely hypoxanthine, is the immediate purine precursor of riboflavine.

L17 ANSWER 180 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1970:19372 CAPLUS <<LOGINID::20100917>>
DN 72:19372
OREF 72:3517a,3520a
TI Simplified method for ***testing*** mutagens in saccharomyces
AU Fink, Gerald R.; Lowenstein, Robert
CS Cornell Univ., Ithaca, NY, USA

SO Journal of Bacteriology (1969), 100(2), 1126-7 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB The reversion frequency of ***auxotrophic*** ***yeast*** mutants was stimulated when the cells were treated with mutagens [N-methyl-N-nitro-N-nitrosoguanidine, 2-methoxy-6-chloro-9-(3-ethyl-2-chloro-ethylaminopropylamino)acridine dihydrochloride, or diethylsulfate] while growing on a growth medium and then placed on selective medium. Cells exposed to mutagen directly on minimal medium showed only the background reversion frequency. The technique may permit the development of a mutant classification scheme in yeast similar to that used in bacteria.
OSC.G 2 THERE ARE 2 CAPLUS RECORDS THAT CITE THIS RECORD (2 CITINGS)

L17 ANSWER 181 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1970:19367 CAPLUS <<LOGINID::20100917>>
DN 72:19367
OREF 72:3517a,3520a
TI Methyl-deficient transfer ribonucleic acid and macromolecular synthesis in methionine-starved Saccharomyces cerevisiae
AU Kjellin-Straby, Kerstin; Phillips, John H.
CS Univ. Uppsala, Uppsala, Swed.
SO Journal of Bacteriology (1969), 100(2), 679-86 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB Haploid methionine ***auxotrophs*** of S. ***cerevisiae*** continue to multiply for several hr after withdrawal of a required amino acid from the medium. Macromol. synthesis continues during this period of residual growth, although the net RNA and protein content is constant during the latter part of this period. In this study, growth after withdrawal of methionine was in some cases accompanied by accumulation of transfer RNA (tRNA), which was shown by methylation in vitro to be deficient in Me groups. This phenomenon was shown by only 4 of 9 methionine auxotrophs ***tested*** , but no evidence could be found that these 4 strains had relaxed control of RNA synthesis. The 9 methionine-requiring strains represent mutations in 5 different positions in the methionine biosynthesis pathway, and only mutants blocked at 2 of these 5 positions accumulated Me deficient tRNA. This accumulation therefore appears to be correlated with the position of the strain's block in the pathway of methionine biosynthesis.

L17 ANSWER 182 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1970:19325 CAPLUS <<LOGINID::20100917>>
DN 72:19325
OREF 72:3508h,3509a
TI Methyl-deficient transfer ribonucleic acid in Saccharomyces cerevisiae
AU Phillips, John H.
CS Univ. Uppsala, Uppsala, Swed.
SO Journal of Bacteriology (1969), 100(2), 695-700 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB Me deficient tRNA is found in certain methionine ***auxotrophs*** of ***Saccharomyces*** ***cerevisiae*** during logarithmic growth (at 1 generation time before the late growth phase) and during residual growth in the ***absence*** of exogenous methionine. The former effect seems to be accounted for by the general increase in RNA synthesis that occurs at the time; there is no specific synthesis of tRNA in the ***absence*** of ribosomal RNA synthesis, nor is the Me group deficiency limited to a single tRNA species. During methionine starvation, all species of tRNA are Me deficient, but this occurs only in strains with certain blocks in the methionine pathway. The kinetics of disappearance of the Me group donor, S-adenosylmethionine, during starvation of D73 (which accumulates Me deficient tRNA) do not differ from other strains, but D73 loses the methylase inhibitor, S-adenosylhomocysteine, much more slowly.

L17 ANSWER 183 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1969:428047 CAPLUS <<LOGINID::20100917>>
DN 71:28047
OREF 71:5165a,5168a
TI Synthesis of dethiobiotin from 7,8-diaminopelargonic acid in biotin auxotrophs of Escherichia coli K-12
AU Eisenberg, Max A.; Krell, Kenneth
CS Coll. of Phys. and Surg., Columbia Univ., New York, NY, USA
SO Journal of Bacteriology (1969), 98(3), 1227-31 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB The synthesis of dethiobiotin from 7,8-diaminopelargonic acid (DAP) was demonstrated in resting cell suspensions of E. coli K-12 bioA mutants under conditions in which the biotin locus was derepressed. The biosynthetically formed dethiobiotin was identified by chromatog., electrophoresis, and by its ability to support the growth of ***yeast*** and those E. coli biotin ***auxotrophs*** that are blocked earlier in the biotin pathway. Optimal conditions for dethiobiotin synthesis were detd. Dethiobiotin synthetase activity was repressed 67% when partially derepressed resting cells were incubated in the ***presence*** of 3 ng. of biotin per ml. Serine, bicarbonate, and glucose stimulated dethiobiotin synthesis apparently by acting as sources of CO2. The results of this study are consistent with an earlier postulated pathway for biotin biosynthesis in E. coli: pimelic acid .fwdarw. 7-oxo-8-aminopelargonic acid .fwdarw. DAP .fwdarw. dethiobiotin .fwdarw. biotin.

L17 ANSWER 184 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1969:26607 CAPLUS <<LOGINID::20100917>>
DN 70:26607
OREF 70:4975a
TI Biosynthesis of branched-chain amino acids in ***yeast*** : regulation of leucine biosynthesis in prototrophic and leucine ***auxotrophic*** strains
AU Satyanarayana, T.; Umbarger, H. Edwin; Lindegren, Gertrude
CS Purdue Univ., Lafayette, IN, USA
SO Journal of Bacteriology (1968), 96(6), 2018-24 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB The 1st enzyme in the biosynthesis of leucine in yeast, .alpha.-isopropylmalate synthetase, is inhibited by L-leucine. In a mutant resistant to the analog 5',5',5'-trifluoroleucine, the enzyme is markedly resistant to inhibition by L-leucine. Growth in the ***presence*** of exogenous L-leucine results in repression of the 2nd and 3rd enzymes of the pathway. The 1st enzyme is not repressed unless both L-leucine and L-threonine are supplied in the medium. Comparison of levels of the

remaining 2 enzymes in leucine auxotrophs grown under conditions of leucine excess and leucine limitation reveals deviations from the wild-type derepression pattern in some mutants. In some, repression of the synthetase by leucine alone was observed. In others, the repressibility of the dehydrogenase was lost. It is unlikely that these deviations were due to the same primary mutational event that caused leucine auxotrophy. No mutants were found in which an altered gene was recognized to be clearly responsible for the level of the leucine-forming enzymes.
OSC.G 3 THERE ARE 3 CAPLUS RECORDS THAT CITE THIS RECORD (3 CITINGS)

L17 ANSWER 185 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1968:400749 CAPLUS <<LOGINID::20100917>>
DN 69:749
OREF 69:139a,142a
TI The induction of biochemical and morphological mutants in the moss, Physcomitrella patens
AU Engel, Paulinus P.
CS Yale Univ., New Haven, CT, USA
SO American Journal of Botany (1968), 55(4), 438-46 CODEN: AJBOAA; ISSN: 0002-9122
DT Journal
LA English
AB Mutants of P. patens, a monoecious, cleistocarpous moss which completes its life cycle under defined conditions in 7-8 weeks, were induced by treatment of either spores or protonemal cells with Et methanesulfonate, N-methyl-N-nitro-N-nitrosoguanidine, or x-rays. Thiamine, p-aminobenzoic acid, niacin, and ***yeast*** ext. ***auxotrophs*** were obtained. In addn., 5 yellow mutants, in which the chlorophyll content was reduced to 35-65% of the wild type, and 2 morphological mutants were also induced. The self-sterility of the p-aminobenzoic acid-dependent mutant seemed to be pleiotropically related to the auxotrophic condition, since self-sterility did not segregate from nutritional dependence in progeny of crosses with a yellow mutant and a morphological mutant. On the basis of ***tests*** with heterozygous diploids obtained by aposporous regeneration of capsule cells, 2 mutant alleles were shown to be recessive to their resp. wild-type alleles. The relatively short life cycle, the ability to do crosses, and the ease in culturing P. patens on a microbiol. scale suggest that this organism may be suitable exptl. material for biochem., genetic, and developmental studies. 34 references.
OSC.G 18 THERE ARE 18 CAPLUS RECORDS THAT CITE THIS RECORD (18 CITINGS)

L17 ANSWER 186 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1968:85204 CAPLUS <<LOGINID::20100917>>
DN 68:85204
OREF 68:16391a,16394a
TI Cystathionine metabolism in methionine ***auxotrophic*** and wild-type strains of ***Saccharomyces*** ***cerevisiae***
AU Sorsoli, Wayne A.; Buettner, Michael; Parks, Leo W.
CS Oregon State Univ., Corvallis, OR, USA
SO Journal of Bacteriology (1968), 95(3), 1024-9 CODEN: JOBAAY; ISSN: 0021-9193
DT Journal
LA English
AB The role of cystathionine in methionine biosynthesis in wild-type and ***auxotrophic*** strains of S. ***cerevisiae*** was studied. Homocysteine and cysteine-requiring mutants were selected for detailed study. Exogenously supplied cystathionine, although actively transported by all strains ***tested*** , could not satisfy the org. S requirements of the mutants. Wild-type and homocysteine and cysteine auxotrophs cell-free exts. were shown to cleave cystathionine. Pyruvic acid and homocysteine were identified as the products of this cleavage. A mutant contg. an enzyme which could cleave cystathionine to homocysteine in cell-free expts. was unable to use cystathionine as a methionine precursor in the intact organisms. The significance of this finding is discussed. 25 references.

L17 ANSWER 187 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1967:471323 CAPLUS <<LOGINID::20100917>>
DN 67:71323
OREF 67:13403a,13406a
TI Regulation of homoserine O-transacetylase, first step in methionine biosynthesis in Saccharomyces cerevisiae
AU De Robichon-Szulmajster, Huguette; Cherest, Helene
CS C.N.R.S., Gif-sur-Yvette, Fr.
SO Biochemical and Biophysical Research Communications (1967), 28(2), 256-62 CODEN: BBRCA9; ISSN: 0006-291X
DT Journal
LA English
AB Cell-free exts. of yeast catalyzed the exchange of 14C from DL-homoserine-14C into synthetic O-acetyl-DL-homoserine, forming O-acetyl-homoserine-14C. S. ***cerevisiae*** , strain D-6, a methionine ***auxotroph*** , grew with the same efficiency and identical yields on methionine, homocysteine, or O-acetylhomoserine; in the ***absence*** of any one of these compds., there was a residual growth corresponding to exhaustion of exogenous methionine, which stopped completely after 4 hrs. Exts. of the mutant strain had no homoserine O-transacetylase (I) activity. In the wild-type yeast, synthesis of I appeared to be dependent upon exogenous DL-methionine concns.; at 2 .times. 10-3M DL-methionine, I synthesis was repressed by about 63%. S-Adenosylmethionine (10-2M) inhibited I activity by 74%. In yeast, the 1st step in methionine biosynthesis is catalyzed by I; exogenous methionine represses the synthesis of this enzyme. 17 references.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

L17 ANSWER 188 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1966:492952 CAPLUS <<LOGINID::20100917>>
DN 65:92952
OREF 65:17419g-h,17420a-c
TI Sorption of some ions by algae related to their nutrition supply conditions
AU Dvorak, M.; Dvorakova-Hladka, Jirina; Fialova, Svatava
CS Karlova Univ., Prague
SO Biol. Plant. Acad. Sci. Bohemoslov. (1966), 8(5), 362-80
DT Journal
LA English
AB Studies were carried out on Scenedesmus obliquus, Chlorella pyrenoidosa, and Coccomyxa solorinae saccatae to det. the effect on the sorption of K+, Ca2+, Zn2+, and PO43- of supplementing Benson's mineral culture medium with glucose or yeast ext. or both. Cultures were considered autotrophic when grown on the unsupplemented mineral medium, heterotrophic when grown on the mineralmedium plus 1% glucose in the dark, and mixotrophic when grown on the same medium in the light. Some cultures were grown on the mineral medium supplemented with i% glucose and 80 ml. yeast ext./1. ***Yeast*** ext. was considered an ***auxotrophic*** supplement. The most rapid

growth of all 3 algae as measured by turbidimetry through a green filter was under mixotrophic conditions. The several algae differed in their responses to supplementation of the media and to the conditions under which they were cultivated before the expts. The ions to be studied were tagged by radioactive isotopes and were detd. by measuring the radioactivity. The centrifuged algal cells were resuspended in 0.0043M MgSO4 for the detn. of the sorption of K+ and in 0.01M KCl + 0.0043M MgSO4 at pH 6 for that of the other ions. Sorption of K+ was 6 .times. 10-9 mole/mg. dry wt. from a culture soln. that contained 0.0004M KCl and 6 .times. 10-8 mole from one that a contained 0.004M KCl in the light for Chlorella after 6 hrs. Similar increases of sorption of K+ with increased K+ concn. was shown under other conditions and by the other algae. After mixotrophic precultivation, the algae showed decreased sorptive capacity. Sorption of K+ was not affected by the ***presence*** of Ca2++ and was increased by increased metabolism. Thus, it was increased by light or supplementation when metabolism was stimulated. The uptake of P from solns. that contained 10-610-2M was positively but not linearly related to the concn. It was stimulated by light but not by supplementation. The ***presence*** of Ca2+ caused nonmetabolic sorption of P. The uptake b of Ca2+ was predominantly adsorption assocd. with the ***presence*** of P. Up to 75% of this Ca2+ could be washed out with 0.001M HCl. The insol. portion increased with the alky. of the medium, esp. above pH 6.5. Org. nutrients had important effects on the formation of the adsorption system. In all expts., the values for Zn3+ were higher than for Ca2+ and the effect of alky. was more pronounced.

L17 ANSWER 189 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1966:484252 CAPLUS <<LOGINID::20100917>>
DN 65:84252
OREF 65:15825e
TI Mutagenic effect of 1-nitroso-3-nitro-1-methylguanidine on Sacchaxomyces cerevisiae
AU Lingens, F.; Oltmanns, O.
CS Univ. Tuebingen, Germany
SO Zeitschrift fuer Naturforschung, Teil B: Anorganische Chemie, Organische Chemie, Biochemie, Biophysik, Biologie (1966), 21(7), 660-3 CODEN: ZENBAX; ISSN: 0044-3174
DT Journal
LA German
AB The no. of ***auxotrophic*** mutants among the surviving cells of S. ***cerevisiae*** increased up to 30% when grown in the ***presence*** of 1-nitroso-3-nitro-1-methylguanidine (20-500 .beta./ml.). These 1-nitroso-3-nitro-1-methylguanidine-induced mutants showed poor growth. The reasons for this poor growth were unclear.

L17 ANSWER 190 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1966:107240 CAPLUS <<LOGINID::20100917>>
DN 64:107240
OREF 64:20266g-h
TI The action of 6-diazo-5-oxonorleucine and albizziine on the biosynthesis of anthranilic acid in Saccharomyces cerevisiae
AU Lingens, Franz; Lueck, Wolfgang; Mueller, Gerhard
CS Univ. Tuebingen, Germany
SO Hoppe-Seyler's Zeitschrift fuer Physiologische Chemie (1966), 343(4-6), 282-9 CODEN: HSZPAZ; ISSN: 0018-4888
DT Journal
LA German
AB 6-Diazo-5-oxonorleucine or albizziine (2-amino-3-ureidopropionic acid) inhibited the synthesis of anthranilic acid by a tryptophan ***auxotroph*** of S. ***cerevisiae*** , resulting in the accumulation of chlorismic acid in the medium; these results were also obsd. with a phe-, tyr- mutant of S. cerevisiae. Wild strains of S. cerevisiae and Escherichia coli released 4-hydroxybenzoic acid and phenylpyruvic acid into the medium in the ***presence*** of 6-diazo-5-oxonorleucine.

L17 ANSWER 191 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1966:53956 CAPLUS <<LOGINID::20100917>>
DN 64:53956
OREF 64:10126e-g
TI Nicotinic acid biosynthesis in prototrophs and tryptophan ***auxotrophs*** of ***Saccharomyces*** ***cerevisiae***
AU Ahmad, Fazal; Moat, Albert G.
CS Hahnemann Med. Coll., Philadelphia, PA
SO Journal of Biological Chemistry (1966), 241(4), 775-80 CODEN: JBCHA3; ISSN: 0021-9258
DT Journal
LA English
AB Yeasts utilize tryptophan for the synthesis of nicotinic acid under aerobic, but not under anaerobic, conditions. Under aerobic conditions of growth, radioactivity from tryptophan-14C uniformly labeled in the benzene ring and 3-hydroxyanthranilic-carboxyl-14C acid is incorporated into nicotinic acid. Under anaerobic conditions, little radioactivity from these compds. is incorporated into nicotinic acid. The ***presence*** of a tryptophan-nicotinic acid pathway in yeast is further supported by the establishment of the ***presence*** of formylkynurenine formamidase and 3-hydroxyanthranilic acid oxidase, 2 of the enzymes known to mediate the conversion of tryptophan to nicotinic acid in mammalian systems. Under anaerobic conditions, yeasts incorporate radioactivity from uniformly labeled aspartate-14C and glutamate-14C, suggesting that an alternative pathway similar to that shown in several bacterial systems is operative. Quinolinic acid is a precursor to nicotinic acid adenine dinucleotide under either aerobic or anaerobic conditions. Quinolinic acid appears, therefore, to be a common intermediate in the alternative pathways for nicotinic acid biosynthesis in yeast.
OSC.G 11 THERE ARE 11 CAPLUS RECORDS THAT CITE THIS RECORD (11 CITINGS)

L17 ANSWER 192 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1966:45467 CAPLUS <<LOGINID::20100917>>
DN 64:45467
OREF 64:8562a-d
TI Some properties of sulfite reductase from yeast
AU Naiki, Nobuo
CS Univ. Gifu, Japan
SO Plant and Cell Physiology (1965), 6(2), 179-94 CODEN: PCPHA5; ISSN: 0032-0781
DT Journal
LA English
AB cf. CA 61, 4747h. The reduced methylviologen (MVH)- and NADPH-linked sulfite reducing activities were assayed in exts. obtained from a wild strain of ***Saccharomyces*** ***cerevisiae*** and various ***auxotrophic*** mutants derived from it. All the exts. possessing the NADPH-linked activity also showed the MVH-linked activity, and all those lacking the latter also lacked the former. However, exts. from several mutants had the MVH-linked activity without having the other. NADPH-sulfite reductase (I) was purified nearly 200-fold from exts. of the wild strain. Throughout the purifn. steps, the MVH-

linked activity was also purified in assocn. with the NADPH-linked activity, and the ratio between the 2 remained essentially const. However, on exposure to heat, low ionic strengths, and p-chloromercuribenzoate, NADPH-linked activity was lost, leaving the MVH-linked activity almost unaffected. Both activities were sensitive to CN-. I could also reduce NO2- and H2NOH, and the NO2- and H2NOH-reducing activity was sensitive to the treatments which inhibited the NADPH-sulfite reducing activity. Addn. of NO2- or H2NOH competitively inhibited the NADPH-linked sulfite redn. I also showed diaphorase activity, reducing 2,6-dichloroindophenol or methylviologen. This activity was inhibited by the treatment to which the NADPH-linked sulfite redn. was sensitive, but it was not sensitive to CN-. A tentative schematic model for yeast sulfite reductase is ***presented*** .

L17 ANSWER 193 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1964:451018 CAPLUS <<LOGINID::20100917>>
DN 61:51018
OREF 61:8865e-h
TI Higher aliphatic alcohols in beer and some factors which quantitatively influence their formation
AU Drews, B.; Specht, H.; Baerwald, G.
CS Tech. Univ., Berlin
SO Monatsschr. Brauerei (1964), 17(6), 101-16
DT Journal
LA Unavailable
AB Higher aliphatic alcs. were sepd. quant. from beer samples by means of 2 successive distns. followed by rectification. The less volatile .beta.-phenylethanol was captured only incompletely by this procedure, accumulating in the final concentrate between 1 and 10%. The higher alcs. were sepd. from the fraction distg. between 79 and 100.degree. by means of 5 extns. with 2:1 ether-pentane. The combined exts. were dried over Na2SO4 and the solvent mixt. removed on a water bath. A modified Komarowski reaction (cf. Duke, CA 41, 7385f) was used to det. total higher aliphatic alcs. The proportion of alcs. detd. in 20 beer samples was: (av. value in parentheses): total alcs. 54-105 mg./l. (74 mg./1.); individual components in the mixt.: PrOH 0.5-22.3 (7.4); iso-BuOH 3.0-19.1 (11.1); amyl alcs. (mixt. of 2-methyl-l-butanol and 3-methyl-l-butanol) 64.8-96.5 (81.9); BuOH, ***present*** in 4 samples only (0.2% by wt.); n-hexanol traces; n-pentanol traces in one sample only. The factors affecting the formation of higher aliphatic alcs. were temp., type of yeast, quantity of yeast, and aeration. A 4-fold starting quantity of yeast and const. agitation in an open vat gave the largest decrease in both fermenting time and amt. of higher ales. (45 mg./1., as compared to 77 mg./l. in a control), without affecting the quality of the product. Fermentation with ***yeasts*** ***auxotrophic*** for leucine or valine-isoleucine (either selected lineages or haploid mutants)also gave variations in the formation of alcs., offering a possibility of influencing their proportion in the product.

L17 ANSWER 194 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1964:62837 CAPLUS <<LOGINID::20100917>>
DN 60:62837
OREF 60:11094h,11095a-d
TI Glutamate ***auxotrophs*** in ***Saccharomyces*** . I. The biochemical lesion in the glt, mutants
AU Ogur, Maurice; Coker, Lowell; Ogur, Sylvia
CS Southern Illinois Univ., Carbondale
SO Biochemical and Biophysical Research Communications (1964), 14(2), 193-7 CODEN: BBRCA9; ISSN: 0006-291X
DT Journal
LA Unavailable
AB Glutamate ***auxotrophs*** of ***Saccharomyces*** are induced (with low frequency) by ultraviolet irradiation. The ***present*** glt1 strain, in addn. to total requirement for glutamate, was also characterized by either poor or negligible growth on media contg. nonfermentable C and energy sources (acetate, lactate, EtOH, glycerol). In crosses to glutamate-independent strains, the dual phenotype segregated as though controlled by a single gene. Selected revertants to glutamate independence (occurring spontaneously with a frequency of approx. 1 in 106 cells, or induced by ultraviolet irradiation), had recovered the ability to utilize nonfermentable substrates, confirming the single gene control of the dual phenotype. To ***test*** whether glt1 strains were also segregational petites, their cytochrome spectra and respiratory ability were examd. The spectral lines of cytochromes a, b, and c were detected in a no. of glt1 strains studied. Cultures of glt1 strains grown in low sugar-lactate broth with agitation for several transfers exhibited strong respiratory capacity with glucose, EtOH, MeCHO, and lactate but failed to respire with acetate. Stoichiometry of O uptake with limiting amts. of EtOH and MeCHO were consistent with oxidation proceeding only to the level of acetate with glt1 strains, whereas GLT strains were able to carry oxidn. beyond this level. The biochem. lesions in the glt1 mutant strains involves the inability to synthesize aconitase and results in a nonfunctional tricarboxylic acid (TCA) cycle. These are the first TCA-cycle mutants described in yeast and represent a second major category of mutants with lesions in the aerobic pathway (the first being the cytochrome deficients). The glt1 (aconitase-less) mutants are capable of respiring with various substrates which are oxidized to the level of acetate but are incapable of degrading 2 C substrates to CO2 via the TCA cycle. The block at aconitase leads to citrate accumulation when glucose is metabolized. The inability to reach .alpha.-ketoglutarate via the TCA cycle is expressed as a total growth requirement for glutamate in the ***presence*** of 18 other common amino acids.
OSC.G 7 THERE ARE 7 CAPLUS RECORDS THAT CITE THIS RECORD (7 CITINGS)

L17 ANSWER 195 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1960:130063 CAPLUS <<LOGINID::20100917>>
DN 54:130063
OREF 54:25011d-f
TI Inhibition by histidine of the prototropic mutation in diploid heteroallelic yeast cells for the locus adenine-histidine
AU Luzzati, Mario; Clavilier, Lea; Slonimski, Piotr P.
SO Compt. rend. (1959), 249, 1412-14
DT Journal
LA Unavailable
AB A microscopic examn. and counting of yeast cells (***Saccharomyces*** ***cerevisiae***) in an agar medium established that the heteroallelic diploid ***auxotrophs*** continue to mutate to the order of 10-4/cells/day; the mutation results from a somatic recombination without noticeable cellular division (cf. Roman, CA 50, 15715f). The mutation precludes a definite metabolism which is diminished in the ***absence*** of glucose, uracil, or when the agar is washed with HCl and pptd. by iso-PrOH, but the addn. of traces of adenine causes a rapid increase in mutations. The addn. of histidine inhibits the mutations, but increases the growth of the residual auxotrophs. Redn. in mutations by adenine is 6 times, adenine and histidine is 150 times, and histidine alone is 500 times/day.

L17 ANSWER 196 OF 196 CAPLUS COPYRIGHT 2010 ACS on STN
AN 1956:82946 CAPLUS <<LOGINID::20100917>>
DN 50:82946
OREF 50:15715g-i,15716a
TI Spontaneous and chemically induced mutations giving rise to canavanine resistance in yeast
AU Srb, Adrian M.
CS Cornell Univ., Ithaca, NY
SO Comptes Rendus des Travaux du Laboratoire Carlsberg, Serie Physiologique (1956), 26, 363-80 CODEN: CRTPAB; ISSN: 0366-810X
DT Journal
LA English
AB Saccharomyces cerevisiae was used for studies of chem. mutagenesis by way of usual techniques of screening for antibiotic resistance. The system involved treatment of canavanine-sensitive cells and scoring for the appearance of canavanine-resistant (I) mutants. Reproducible results valid for comparative purposes were obtained, but precise numerical treatment was not achieved because of the ***presence*** of cell clusters in haploid cultures. The recovery of I mutants out of populations of sensitive cells was approx. quant. Reconstruction expts. or diln. series did not reveal "Grigg effects" or other kinds of plating interactions. Neither did the device of inoculating treated and untreated cells into the same plates. This latter device revealed a striking interaction between prototrophs and adenine-requiring ***auxotrophs*** of ***yeast*** . I mutants were produced more effectively with .beta.-propiolactone than with .gamma.-butyrolactone or .gamma.-valerolactone. A presumably typical I mutant behaved as a recessive in a cross with a sensitive strain. Analysis of asci formed by the sporulating hybrid showed 2:2 segregations for sensitivity. After treatment with .beta.-propiolactone, certain sensitive heterozygous diploids gave an appreciably higher frequency of I mutants than did haploid sensitives or homozygous diploid sensitives.
OSC.G 1 THERE ARE 1 CAPLUS RECORDS THAT CITE THIS RECORD (1 CITINGS)

=> d his
(FILE 'HOME' ENTERED AT 12:04:56 ON 17 SEP 2010)
FILE 'CAPLUS' ENTERED AT 12:05:31 ON 17 SEP 2010
L1 7899 S AUXOTROPH?/BI,AB
L2 7638966 S (PRESEN? OR ABSEN? OR TEST?)/BI,AB
L3 2881 S L1 AND L2
L4 632 S L3 AND (YEAST? OR SACCHAROMYCES OR CEREVISIAE)/BI,AB
L5 614 S L4 NOT 2010/PY
L6 591 S L5 NOT 2009/PY
L7 569 S L6 NOT 2008/PY
L8 547 S L7 NOT 2007/PY
L9 840 S (AUXOTROPH? (10A) (YEAST? OR SACCHAROMYCES OR CEREVISIAE))/BI
L10 271 S L2 AND L9
L11 261 S L10 NOT 2010/PY
L12 252 S L11 NOT 2009/PY
L13 242 S L12 NOT 2008/PY
L14 234 S L13 NOT 2007/PY
L15 222 S L14 NOT 2006/PY
L16 208 S L15 NOT 2005/PY
L17 196 S L16 NOT 2004/PY

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